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PubMed=14760490;
Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
Irwin J.A., Parsons T.J.;
"Single nucleotide polymorphisms over the entire mtDNA genome that
increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
-:- FUNCTION: This is one of the chains of the nonenzymatic component
(CF(0) subunit) of the mitochondrial ATPase complex (By
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Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
Irwin J.A., Parsons T.J.;
Single nucleotide polymorphisms over the entire mtDNA genome that
increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
Int. J. Legal Med. 0:0-0 (2004).
(CP(0) subunit) of the mitochondrial ATPase complex (By
                                                                                                                                                                                                                                                                                                                                            c -i- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate + H(+)(but).

c -i- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate + H(+)(but).

c -i- SUBCELLULAR LOCATION: Membrane-bound (By similarity).

c -i- SIMILARITY: Belongs to the ATPase protein 8 family.

R EMBL; AY495283; AAR95009.1; -..

R GO; 00:005739; Cantuchondrion; IEA.

InterPro; IRR001411; ATPASSE mit.

R GO; 00:005739; Cantuch 8; 1.

R Ffam; PP00895; ATP-synt 8; 1.

KW CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;

KW Transmembrane; Transport.

SQ SEQUENCE 68 AA; 7966 MW; 7D307ES13ACB0546 CRC64;
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Watszycza, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
VCBI_TaxID=9606,
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-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate H(+)(Out).
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-! SIMILARITY: Belongs to the ATPase protein 8 family.
BEMEL, AX495258; AAR94684.1; ...
GO, GO: 0005739; C.mitochondrion; IEA.
InterPro; IPR001421; ATPase8 mit.
Pfam; PF00895; ATP-synt 8; 1.
CF(0); Hydrogen ion transport; Ion transport; Mitochondrion; SEQUENCE 68 AA; 7982 MW; COA07E513AD76935 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATP synthase F0 subunit 8.
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SEQUENCE FROM N.A.
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"Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
-!- FUNCTION: This is one of the chains of the nonenzymatic component (CF(0) subunit) of the mitochondrial ATPase complex (By
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-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(1n) = ADP + phosphate +
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Mitochondrion.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TAXID=9606;
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-:- SUBCELLUIAR LOCATION: Membrane-bound (By similarity).
-:- SUBLETLUIAR LOCATION: Membrane-bound (By similarity).
-:- SIMILARITY: Belongs to the ATPase protein 8 family.
-:- SMB1, AV495321; AR955031; -:- GO. GO.0005739; C:mitochondrion; IEA.
InterPro; IPR001421; ATPase8 mit.
Pfam; PF00895; ATP-synt 8; 1.
Pfam; PF00895; ATP-synt 8; 1.
Transmembrane; Transport; Ion transport; Mitochondrion;
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                                                                                                                    Length 68;
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Last annotation update)
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Best Local Similarity 69.0%; Pred. No. 2.2e-06;
Matches 20; Conservative 6; Mismatches 2;
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EMBL; AY339510; AAP90444.1; -. EMBL; AY339511; AAP90457.1; -.
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Homo sapiens (Human).

Mitochondrion.
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QGRKZ6;
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-!- SINCELLULAR LOCATION: Membrane-bound (By similarity).
-!- SINILARITY: Belongs to the ATPase protein 8 family.
-!- SINILARITY: Belongs to the ATPase protein 8 family.
BMBL; AX253166, AA06051.1; -.
GO, GO:0005739; C:mitochondrion; IEA.
GO, GO:0016469; C:mitochondrion; IEA.
GO, GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
GO, GO:0016591; F:hydrogen-transporting ATPase activity. .; IEA.
GO, GO:0015986; P:ATP synthesis coupled proton transport; IEA.
GO, GO:0015986; P:ATP synthesis coupled proton transport; IEA.
InterPo: IPR001421; ATPase8 mit.
Pfen; PF00895; ATP-synt 8; 1.

EF(0): Hydrogen ion transport; Ion transport; Mitochondrion;
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-!- SUBLIARITY: Belongs to the ATPase protein 8 family.
-!- SMILARITY: Belongs to the ATPase protein 8 family.
EMBL; AY289079; AAP48248.1;
GO; GO:0005739; Camtcochondrion; IEA.
GO; GO:0014699; Ciproton-transporting two-sector ATPase complex; IEA.
GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. . ; IEB.
GO; GO:0046961; F:hydrogen-transporting ATPase activity, rota. . ; IEA.
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Ingman M., Gyllensten U.;
"Mitochondrial genome variation and evolutionary history of Australian
                                                                                                         PubMed=12949126;
Moilanen J.S., Finnila S., Majamaa K.;
Moilanen J.S., Finnila S., Majamaa K.;
Milneage-specific selection in human mtDNA: lack of polymorphisms in segment of MTND5 gene in haplogroup J.";
Mol. Biol. Evol. 20:133-2142(3003).

-i- FUNCTION: This is one of the chains of the nonenzymatic component (CF(0) subunit) of the mitochondrial ATPase complex (By
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Genome Res. 13:1600-1606(12003).
-!- FUNCTION: This is one of the chains of the nonenzymatic component (CF(0) subunit) of the mitochondrial ATPase complex (By
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-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
H(+)(Out).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEGUENCE 68 AA, 8002 MW; 7FE07E513AD76936 CRC64;
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69.0%; Pred. No. 2.2e-06;
iive 6; Mismatches 2;
Finnila S., Lehtonen M.S., Majamaa K.;
"Phylogenetic network for European mtDNA.";
Am. J. Hum. Genet. 68:1475-1484(2001).
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Matches 20, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Q7YEE7
    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T., Irwin J.A., Parsons T.J., "Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians.", Int. J. Legal Med. 0:0-0(2004).

-!- FUNCTION: This is one of the chains of the nonenzymatic component (CF(0) subunit) of the mitochondrial ATPase complex (3y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kong Q.-P., Yao Y.-G., Sun C., Bandelt H.-J., Zhu C.-L., Zhang Y.-P., "Phylogeny of East Asian Mitochondrial DNA Lineages Inferred from Complete Sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Cararrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SÜBCELLÜLAR LOCATION: Membrane-bound (By similarity).
-1- SINILARITY: Belongs to the ATPase protein 8 family.
BEMBL, AY495226; AR8942681; -.
GO; GO:0005739; C:mitochondrion; IBA.
InterPro; IPR001421; ATPases@ mit.
Pfam; PR00895; ATPsaynt 8; 1.
CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;
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                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                  68 AA
2 RINTTVWPTIITPILLTLFLITN-RLITT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 QLNTTVWPTMITPMLLTLFLITQLKMLNT 31
                                                                                                                                                                            Created)
                                                                                                                                  PRT;
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SEQUENCE FROM N.A.
MEDLINE=21313109; PubMed=11349229;
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                                                                                                                                                                        05-JUL_2004 (TrEMBLrel. 27, 05-JUL_2004 (TrEMBLrel. 27, 05-JUL_2004 (TrEMBLrel. 27, ATP synthase F0 subunit 8.
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                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=14760490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity)
                                                                                                                                                                                                                                                                                                             Mitochondrion.
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                                                                                                                                                                                                                                                                   Name=ATP8;
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Best Local &
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Q7YCD6

RESULT 6

Matches

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Q7YEG9

Matches

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SEQUENCE FROM N.A.
MEDLINE-22406325, PubMed=12509511;
Mishmar D., Ruiz-Peenini E., Golik P., Macaulay V., Clark A.G.,
Mishmar D., Brandon M., Easley K., Chen E., Brown M.D.,
Sukernik R.I., Olckers A., Wallace D.C.;
"Natural selection shaped regional mtDNA variation in humans.";
Proc. Natl. Acad. Sci. U.S.A. 100:171-176(2003).
-:- FUNCTION: This is one of the chains of the nonenzymatic component
(CF(0) subunit) of the mitochondrial ATPase complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1. SINCELLULAR LOCATION: Membrane-bound (By similarity).
-1. SIMILARITY: Belongs to the ATPase protein 8 family.
EMB1, AN195782; AAO88765.11.
GO; GO:0005739; Camitochondrion; IEA.
GO; GO:0016469; C:proton-transporting two-sector ATPase complex; ISO; GO:0046931; F:hydrogen-transporting ATP synthase activity.
GO; GO:0046931; F:hydrogen-transporting ATPase activity.
GO; GO:0015986; P:hydrogen-transporting ATPase activity.
GO; GO:0015992; P:proton transport; IEA.
Interpro; IPR001421; ATPase mit.
Pfam; PF00895; ATP-SYLE 8; 1.

Pfam; PF00895; ATP-SYLE 8; 1.

GT(0); Hydrogen ion transport; Ion transport; Mitochondrion;
                                                                                                                                                              Mitochondrion.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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--- CATALYIC ACTIVITY: ATP + H(2)O + E(+)(In) = ADP + phosphate
H(+)(Out).
-!- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
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MEDLINE=22406325; PubMed=12509511;
Mishmar D., Ruiz-Peeini E., Golik P., Macaulay V., Clark A.G.,
Mishmar D., Ruiz-Peeini E., Golik P., Macaulay V., Clark A.G.,
Mishmar D., Ruiz-Peeini E., Golik P., Chen E., Brown M.D.,
Sukernik R.I., Olckers A., Wallace D.C.,
"Natural selection shaped regional mtDNA variation in humans.";
Proc. Natl. Acad Sci. U.S.A. 100:171-176(2003).
-!- FUNCTION: This is one of the chains of the nonenzymatic comp
(CF(0) subunit) of the mitochondrial ATPase complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 AA; 8012 MW; C0D77E513AD7692B CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ATP synthase F0 subunit 8.
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ATP synthase F0 subunit 8.
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                                        ATP synthase F0 subunit
                                                                                                                  Homo sapiens (Human).
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Q85KZ3
            SO WENT THE PRESENCE OF THE PR
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MEDLINES 2273755; PubMed=12840039;

MEDLINES 2273755; PubMed=12840039;

Ingman M., Gyllensten U.;

"Mitochondrial genome variation and evolutionary history of Australian and New Guinean aborigines.";

Genome Res. 13:1600-1606(2003).

-!- FUNCTION: This is one of the chains of the nonenzymatic component (CP(0) subunit) of the mitochondrial Arpase complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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GO; GO: 0015986; P:ATP synthesis coupled proton transport; IEA. GO; GO: 0019992; P:proton transport; IEA. InterPro; IPR001421; ATP8688 mit. Pfo0895; ATP-synt_8; 1. CF(0); Hydrogen ion transport; Ion transport; Mitochondrion; Eransmembrane; Transport. Ion transport; Mitochondrion; ERQUENCE 68 AA; 7962 MW; 7D307E512AD66936 CRC64;
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                                                                                                                                                                                                                                                                                                             68;
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Pred. No. 2.2e-06;
6; Mismatches 2; Indels
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Last annotation update)
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69.0%;
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69.0%;
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01-0CT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
ATP synthase F0 subunit 8.
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Best Local Similarity 69.0'
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                              Local Similarity 69.0
hes 20; Conservative
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                                                                                                                                                                                                                                                                                                             Query Match
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DB 2; Length Indels component

Q85KTS

RESULT 9
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20; Conservative
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AAL54388;
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Q94P44;
                                                              RESULT 12
094744
AC 094744
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AC 094744
DT 01-DBW
DT 01-DBW
DT 05-UM
DT 05-UM
OC MANAMA
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AAC AALS4
AC AALS4
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-: SUBCELLULAR LOCATION: Membrane-bound (By similarity).
-: SUBCELLULAR LOCATION: Membrane-bound (By similarity).
-: SIMILARITY: Belongs to the ATPase protein 8 family.
EMBL; AF465960; AAN14749.1; --
GO, GO:0005739; C:mitochondrion; IEA.
GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
GO; GO:0046931; F:hydrogen-transporting ATP synthase activity. ..; IEA.
GO; GO:0046931; F:hydrogen-transporting ATPase activity, rota. ..; IEA.
GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
GO; GO:0015929: P:proton transport; IEA.
InterPro; IPRO01421; ATPase8 mit.
                    EMBL, AX195756, AAO88427.1,

GO; GO: 0005739; C:mitochondrion; IEA.

GO; GO: 0016469; C:proten-transporting two-sector ATPase complex; IEA.

GO; GO: 00164693; F:hydrogen-transporting ATP synthase activity. .; IEA.

GO; GO: 0016961; F:hydrogen-transporting ATPase activity. .; IEA.

GO; GO: 0015996; P:hydrogen-transporting ATPase activity, rota.

GO; GO: 0015992; P:proten transport; IEA.

GO; GO: 00119912; ATPase8_mit.
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"Mitochondrial genome diversity of Native Americans supports a single early entry of founder populations into America.";
Am. J. Hum. Genet. 71:187-192(2002).
-1- FUNCTION: This is one of the chains of the nonenzymatic component (CF(0) subunit) of the mitochondrial ATPase complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDDINE=2206253; PubMed=12022039;
Silva W.A. Jr., Bonatro S.L., Holanda A.J., Ribeiro-Dos-Santos A.K.,
Patxao B.M., Goldman G.H., Abe-Sandes K., Rodriguez-Delfin L.,
Barbosa M., Paco-Larson M.L., Petzl-Erler M.L., Valente V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
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Pfam, PF00095; ATP-synt 8; 1.

CF(0); Hydrogen ion trainsport; Ion transport; Mitochondrion; Transmembrane; Transport.

REOUENCE 68 AA; 8008 MW; 6C756A113AD76936 CRC64;
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Pred. No. 2.2e-06;
6; Mismatches 2; Indels 1
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CF(0); Hydrogen ion transport; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.3%; Score 102.5; DB 2; Length 69.0%; Pred. No. 2.2e-06; ive 6; Mismatches 2; Indels
SIMILARITY: Belongs to the ATPase protein 8 family
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RENTTVWPTIITPILLTLFLITN-RLITT 29
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Conservative
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01-MAR-2003 (TrEMBLrel. 23,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 69.v.
Thes 20; Conservative
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Homo sapiens (Human).
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01-JUN-2003
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Matches
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Ingman M., Kaessmann H., Paabo S., Gyllensten U.;
Ingman M., Kaessmann H., Paabo S., Gyllensten U.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This is one of the chains of the nonenzymatic component
-(CF(Q) subunit) of the mitochondrial ATPase complex (By
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Maca-Meyer N., Gonzalez A.M., Larruga J.M., Flores C., Cabrera V.M.;
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SEQUENCE FROM N.A.
MEDLINE=21012016; PubMed=11130070;
Ingman M., Kaeesmann H., Paabo S., Gyllensten U.;
Ingman M., Kaeesmann H., Paabo S., Gyllensten U.;
"Mitochondrial genome variation and the origin of modern humans.";
Nature 408:708-713(2000).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606,
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Pfam; PF00895; ATP-synt 8; 1.
CF(0); Hydrosgen ion transport; Ion transport; Mitochondrion;
Transmembrane; Transport.
SEQUENCE 68 AA; 7965 MW; 7D307E512A3967C6 CRC64;
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Pred. No. 2.2e-06;
6; Mismatches 2; Indels
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                                                                                                   SEQUENCE FROM N.A.
Cabrera V.M., Maca-Meyer N., Gonzalez A.M., Larruga J.M., Flores C.;
Subitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF381981; AAL54388.1; ...
Mitcohondrion.
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PubMed=1155319;
Maca-Meyer N., Gonzalez A.M., Larruga J.M., Flores C., Cabrera V.M.;
Major genomic mitochondrial lineages delineate early human
expansions.";
EMC Genet. 2:13-13 (2001).
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Cabrera V.M., Maca-Meyer N., Gonzalez A.M., Larruga J.M., Flores C.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF381983; AAL5414.1; -.
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Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

NCBL TaxID=9606,
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"Major genomic mitochondrial lineages delineate early human expansions."; \rm BMC\ Genet.\ 2:13-13(2001) ,
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SEQUENCE FROM N.A.
PubMed=11553319;
Maca-Meyer N., Gonzalez A.M., Larruga J.M., Flores C., Cabrera V.M.;
Major genomic mitochondrial lineages delineate early human
expansions.";
BMC Genet. 2:13-13(2001).
                                                                                                                                                                                   SEQUENCE FROM N.A.
Cabrera V.M., Maca-Meyer N., Gonzalez A.M., Larruga J.M., Flores C.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF381984; AAL54427.1; -.
Mitochondrion.
SEQUENCE 68 AA; 7992 MW; 7D307E513AD76936 CRC64;
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Matches 20; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

November 10, 2004, 12:32:37; Search time 8.981 Seconds (without alignments) 191.991 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-092-750-28 127 1 TLYLKLTALAVTFLGLLTALDLNYPT 26 Title: Perfect score: 1 Sequence:

Scoring table:

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478139 Total number of hits satisfying chosen parameters:

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Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Database :

Issued Patents AA:*
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2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query	Query				
No.	Score	Match		DB	ID	Description	
н	112	æ	603	٣	US-09-097-889-23	Sequence 23, Appl	
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22	45	35.4	67	4,	US-09-270-767-35719	35,	
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24	45		137	4	-09-452-239-	34, App	
25	4.5	35.4	171	4	-09-248-796A	~`	
26	45	35.4	425	4,	89-0	Sequence 8439, Ap	
27	45	35.4	426	4	-09-583-110-	equence 4783,	

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1 The Page 1-23  The No. 6218117  RAL INFORMATION: PLICANT: Hermstadt, Corrina PLICANT: Hermstadt, Corrina PLICANT: Ghosh, Sountra S. PLICANT: Ghosh, Sountra S. PLICANT: Davis, Robert E. TIES OF INVENTION: ACRIVESTITIONS AND METHODS TIES OF INVENTION: EXTRAMITOCHONDRIAL DNA: WHERE FOR SEQUENCES: 26 ADDRESSEE: SEED and BERRY LLP STREET: 6300 COlumbia Center, 701 Fifth Avo COUNTRY: USA COMPUTRY: USA MEDICATION TYPE: PLOPEY disk MEDICATION TYPE: PLOPEY disk MEDICATION TYPE: PLOPEY ASSETTION: MEDICATION WHERE: US/09/097,889 FILING DATE: 15-001.998 CLASSIFICATION NUMBER: 060088.417 LECOMMUNICATION NUMBER: 660088.417 LECOMMUNICATION NUMBER: 660088.417 LECOMMUNICATION NUMBER: 660088.417 LECOMMUNICATION NUMBER: 660088.417 LECOMMUNICATION NUMBER: 65031 RMATION POR SEQ ID NO: 23: CUENCET RARACTERISTICS: LENGTH: 603 amino acids TYPE: amino acid TYPES TABBERS TOPOLOGY: linear	Score 112; Pred. No. 0; Mismatc	LNYPT       LNYLT
-23 FEGRATION: T: Herrnstadt, Corrina T: Ghosh, Soumitra S. T: Davis, Robert E. TINVENTION: COMPOSITION: INVENTION: AGENTS THAT INVENTION: BETRAMITOCH(SEE) SEE: SEED and BERRY LLF Seattle Compatible TY: G30 Columbia Center, Seattle FORM: RASHINGTON WASHINGTON WASHINGTON TY: USA SEE: SEED AND SERS: SEE: SEED AND SERS: SEE: SEED AND SERS: TYPE: Ploppy disk TYPE: Ploppy disk TREADABLE FORM: TATON NUMBER: US/09/097, TOATION NUMBER: US/09/097, TOATION NUMBER: US/09/097, TOATION NUMBER: 43.55 AGENT INFORMATION: ATION NUMBER: 43.55 AGENT INFORMATION: CONDE: (206) 682-6031 N FOR SEQ ID NO: 23: CHARACTERISTICS: THE SEQ ID NO: 23: THE SEC ID	0 28 % 0 % % 0 %	LYLKLTALAVTFLGLLTALDLNYPT                    LYLKLTALAVTFLGLLTALDLNYLT
197-889-23 RAL INFORMATION: E NO. 621817 RAL INFORMATION: ELICANT: Hernateadt, Corr FLICANT: Ghosh, Soundtra FLICANT: Bavis, Robert E. FLICANT: Bavis, Robert E. TLE OF INVENTION: COMPOSITE OF INVENTION: EXTRAMI MERR OF SCUENCES: 26 RRESPONDENCE ADDRESS: 26 ADDRESSE: SEED and BERRY STREET: Gastle COUTRY: Seatle COUTRY: BASHINGTON CONFUTER: PATCHITL Releas FRENT APPLICATION DATA: APPLICATION NUMBER: US/09 CLASSIFICATION UND US/09 COUTRY CO	88.2%; larity 96.0%; Conservative	FELGE FFLGE FFLGE
1 no. 6218117 RAL INFORMATION: FLICANT: Herrnetadt, FLICANT: Ghosh, Soum PLICANT: Ghosh, Soum COUNTION: ACCOUNTION: ACCOUNTION ACCOUNTION: ACCOUNTION A	rity iserva	ALAV
SUPPLIED BY A STANDARD BY A ST	넡	YLKE YLKE
1 97-889-23 67-889-23 FUGGATT Her PLICANT: Her PLICANT: Her PLICANT: Day PLICANT: Day PLICANT: Day PLICANT: Day PLICANT: Day PLICANT: Day PLICANT: Day PLICANT: Day COUNTRY: USA COUNTRY: USA COUNTR	cch al Sir 24;	2 2 1 484 I
о во в д с о одинидарво	Query Match Best Local Matches 2	4.
USESUCION CONTRACTOR C	Que; Best Matc	공 중 음
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686 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-768-301-4
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US-08-137-614A-16
i Sequence 16, Application US/08137614A
; Patent No. 5487976
i GENERAL INFORMATION:
i APPLICANT: Knipple, Douglas C.
i APPLICANT: Knipple, Douglas C.
i TITLE OF INVENTION: Gene Encoding An Insect
i TITLE OF ENVENTION: Gamma-Aminobutyric Acid (GABA) Receptor Subunit
i CORRESPONDENCE ADDRESS:
i ADDRESSEE: Nixon, Hargrave, Devans & Doyle
synebr: Clinton Square, P.O. Box 1051
i CITY: Rochester
i STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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                                                                                 Sequence 23, Application US/09088079

Patent No. 6489095

GENERAL INFORMATION:

APPLICANT: Herrnstadt, Corrina

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Clevenger, William

APPLICANT: Davis, Roin F.

APPLICANT: Davis, Robert E.

TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA

ZIP: 98104

COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-JUN-1998
CLASSIFICATION + 435
ATTORNEY/AGENT INFORMATION:
NAME: ROSENMAN Ph.D., Stephen J.
REFERENCY DOCKET 1000 NUMBER: 660088.416
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-603
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TELENTH: 603 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                        E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LYLKLTALAVTFLGLLTALDLNYPT 26
                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-09-098-079-23
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Sequence 6, Application US/09617594A

Sequence 6, Application US/09617594A

Sequence 6, Application US/09617594A

Sequence 6, Application US/09617594A

GENERAL INFORMATION:

TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT VI-

TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT VI-

FILE REFERENCE: 454313-3151.1

CURRENT APPLICATION NUMBER: 60/193,332

PRIOR APPLICATION NUMBER: 60/193,332

PRIOR APPLICATION NUMBER: France 99 09421

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 1999-07-16

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.0

SEQ ID NO 6

LENGTH: 625
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                                                                                             Sequence 2, Application US/09583545
Sequence 2, Application US/09583545
Patent No. 6497883
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PORCINE CIRCOVIRUS RECOMBINANT POXVIRUS VACCINE FILE REPERENCE: 454313-2511.1
CURRENT APPLICATION NUMBER: US/09/583,545
CURRENT PILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.
LENGTH: 625
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37.8%; Score 48; DB 4; Length 625;
Best Local Similarity 45.5%; Pred. No. 35;
Matches 10; Conservative 4; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
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Pred. No. 35;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 LYSKKDISAKRFIGLFTSVDIN 517
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Best Local Similarity 45.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: canarypox virus
US-09-617-594A-6
                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Canarypox virus
US-09-583-545-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-452-239-28
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US-09-543-681A-5886

Sequence 5886, Application US/09543681A

Patent No. 6665709

GENERAL INFORMATION

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DATE: 2000-04-05

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5886

LENGTH: 525

TYPE: PRT

CRANISM: Proteus mirabilis

US-09-543-681A-5886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INVERNATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4501
LENGTH: 340
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37.8%; Score 48; DB 4; Length 525;
Best Local Similarity 45.5%; Pred. No. 29;
Matches 10; Conservative 5; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                 .,
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38.2%; Score 48.5; D
Best Local Similarity 52.2%; Pred. No. 33;
Matches 12; Conservative 2; Mismatches
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; Sequence 4501, Application US/09328352
; Patent No. 6562958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4501
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
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US-08-768-301-4
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TP1-07-0C/-760-0T-8D

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APPLICANT: M nryl, Arja
APPLICANT: Wehmaanper , Jari
APPLICANT: Pagerstr m, Richard
APPLICANT: Lanto, Raija
APPLICANT: Lanto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Pirkko
APPLICANT: Lahtinen, Tarja
NITILE OP INVENTION: Production and Secretion of Proteins of NUMBER OF SEQUENCES: 39
                                                                                                                                        Query Match

37.0%; Score 47; DB 2; Length 480;
Best Local Similarity 41.7%; Pred. No. 37;
Matches 10; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1050.0340003
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FILING DATE: 26-0AN-1996
CLASSIFICATION: 536
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-0UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/332,412
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-0CT-1994
CLASSIFICATION: 536
PRICR APPLICATION: 536
PRICR APPLICATION: 536
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APPLICATION WHERE:
FILING DATE:
CLASSIPICATION:
536
ATTORNEY/AGENT INFORMATION:
NAME:
BUGAISKY, LAWENCE B.
REGISTRATION NUMBER:
35,086
REGISTRATION NUMBER:
TELEPHONE:
COSTANTON TRYCOMMATRICON:
TELEPHONE:
202-371-2600
                                                                                                                                                                                                                                                                           2 LYLKLTALAVTFLGLLTALDLNYP 25
                                                                                                                                                                                                                                                                                                                 18 LYRALAAATVSVVGVVTALTVTQP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-590-563-5; Sequence 5, Application US/08590563; Patent No. 6300114; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
   ; MOLECULE TYPE: peptide
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: AM50
US-08-468-812-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
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CHROMOSOME/SEGMENT: AM50-590-563-5
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Vehmaanper, Jari
APPLICANT: Wint Arja
APPLICANT: Mityl, Arja
APPLICANT: Fagerstr m, Richard
APPLICANT: Bantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Paloheimo, Pirko
APPLICANT: Lahtinen, Pirko
APPLICANT: Kristo, Paula
APPLICANT: Kristo, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: Actinomadura 20 E Use
                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                    37.0%; Score 47; DB 4; Length 238; 47.8%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
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CUDNIETS: U.S.A.

CUDNIETS: U.S.A.

ED005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,812
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
FILING DATE: 31-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/32,412
FILING DATE: 320-JUL-1994
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,086
REFRENCE/DOCKET NUMBER: 35,086
REFRENCE/DOCKET NUMBER: 1050.0340002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: STERNE, KESSLER, GOLSTEIN & FOX
1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION WURBER: 60/110,594
EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
SEQ ID NO 28
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |||| : | :||:| | 86 LLLTALNIPHDGKITAIDINRKT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LKLTALAVTFLGLLTALDLNYPT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-468-812-5
; Sequence 5, Application US/08468812
; Patent No. 5935636
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 480 amino acids TYPE: amino acid STRANNEDNESS: not relevant inear
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 47.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
US-09-452-239-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
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GENERAL INFORMATION:
APPLICANT: M ntyl, Arja
APPLICANT: Vehmaanper 'jari
APPLICANT: Lantto, Raija
APPLICANT: Lantto, Raija
APPLICANT: Lantto, Raija
APPLICANT: Lantto, Raija
APPLICANT: Lahtinen, Pirkko
TILLE OF INVENTION: Pirkko
TILLE OF INVENTION: Poduction and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE. FROSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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37.0%; Score 47; DB 4; Length 480;
Best Local Similarity 41.7%; Pred. No. 37;
Matches 10; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,832
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100 New York Ave., N.W. Suite 600 CITY: Washington YOUNDERS STATE D.C. COUNTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLIANTON NUMBER: US/08/590,563
FILING DATE:
CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLIANTON NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
APPLIANTON NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
PRIOR APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: BUGALSKY, LAWFENCE B.
REGISTRATION NUMBER: 1050.0340003
TELECOMMUNICATION NUMBER: 1050.0340003
TELECOMMUNICATION NUMBER: 1050.0340003
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 6667170 Relevant
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  2 LYLKLTALAVTFLGLLTALDLNYP 25
                        18 LYRALAAATVSVVGVVTALTVTQP 41
                                                                                                                                                     Sequence 5, Application US/09235832
Patent No. 6667170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 480 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-235-832-5
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                                                                                                                                                                                                                                                                                                                  APPLICANT: MINING, Arja
APPLICANT: Vehmaanper, Jari
APPLICANT: Vehmaanper, Jari
APPLICANT: Fagersetr m, Richard
APPLICANT: Lantto, Marja
APPLICANT: Paloheimo, Marja
APPLICANT: Lahtinen, Pirkko
APPLICANT: Lahtinen, Tarja
ITILE OF INVENTION: 39
CORRESPONDENCES: 39
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37.0%; Score 47; DB 4; Length 480;
Best Local Similarity 41.7%; Pred. No. 37;
Matches 10; Conservative 5; Mismatches 9; Indels
    Length 480;
                                              9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 New York Ave., N.W. Suite 600 CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTER TEADABLE FORM:
MEDIUTER READABLE FORM:
MEDIUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
Query Match 37.0%; Score 47; DB 3; Best Local Similarity 41.7%; Pred. No. 37; Matches 10; Conservative 5; Mismatches 5
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-0CT-1994
CLASSIFICATION NUMBER: US 08/332,412
FILING DATE: 31-0CT-1994
CLASSIFICATION NUMBER: US 08/282,001
FILING DATE: 29-UDL-1994
CLASSIFICATION:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-UDL-1994
CLASSIFICATION:
APPLICATION NUMBER: 35,086
REGISTRATION NUMBER: 35,086
REGISTRATION NUMBER: 35,086
REGISTRATION NUMBER: 1050.034000
TELECOMMUNICATION NUMBER: 1050.034000
TELECOMMUNICATION NUMBER: 1050.034000
TELECOMMUNICATION NUMBER: 1050.034000
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TYPE: amino acid
STRANDEDNESS: No. 6506593 Relevant
                                                                                          2 LYLKLTALAVTFLGLLTALDLNYP 25
                                                                                                                        18 LYRALAAATVSVVGVVTALTVTQP 41
                                                                                                                                                                                                                                                  Sequence 5, Application US/09770621 Patent No. 6506593 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-09-770-621-5
                                                                                                                                                                                                           RESULT 12
US-09-770-621-5
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Sequence 7, Application US/08468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vehmanper, Jari
APPLICANT: Fagerstr m, Richard

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                           APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Suominen, Tarja
APPLICANT: Kristo, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Pacentine
COMPUTER: Pacenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.0%; Score 47; DB 2; Best Local Similarity 41.7%; Pred. No. 38; Matches 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   GOLSTEIN & FOX N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: November 10, 2004, 13:44:02 Job time : 9.981 secs
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                                                                                                                                                                                                                                                                                                                                                                                   1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
Lantto, Raija
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: STERNE, STREET: 1100 New YOUTY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
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Sequence 241860, Sequence 4898, Ap Sequence 635, Sequence 635, Sequence 635, App Sequence 146138, Sequence 191, App Sequence 191, App Sequence 53, App Sequence 53, App Sequence 53, App Sequence 6478, App Sequence 13, App Sequence 18, App Sequence 1838, App Sequence 1838, App Sequence 62, App Sequence 63, App Sequence 64, App Se

5 US-10-425-115-323215
5 US-10-324-559-241860
10-10-325-277-4898
5 US-10-335-977-4898
7 US-10-325-977-4898
6 US-10-425-114-5296
7 US-10-425-114-5296
6 US-10-424-559-146138
6 US-10-424-559-146138
6 US-10-424-559-146138
6 US-10-724-208-20
7 US-10-724-208-20
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7 US-10-724-208-20
8 US-10-127-33
9 US-10-834-18
9 US-10-129-834-18
9 US-10-129-834-18
9 US-10-129-834-18
9 US-10-134-6508-652
9 US-10-343-6508-652

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-10-092-750-28
 Sequence 28, Appl
Sequence 13, Appl
Sequence 1489, Ap
Sequence 2681, Ap
Sequence 2681, Appl
Sequence 16, Appl
Sequence 1832, Ap
Sequence 16, Appl
                                                                                        November 10, 2004, 16:36:12; Search time 27.9309 Seconds (without alignments) 328.807 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*

| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_Pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO8_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUB.pep:*
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            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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6 US-09-098-079-23

6 US-10-408-765A-1487

6 US-10-408-765A-1489

6 US-10-408-765A-1689

6 US-10-205-219-71

4 US-10-205-219-71

4 US-10-202-798-1488

5 US-10-37-208-16

7 US-10-770-127-187

5 US-10-437-963-198410
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                                                                                                                                                                                                                                     1566620 seqs, 353225886 residues
                                                                                                                                                                     1 TLYLKLTALAVTFLGLLTALDLNYPT 26
                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Query
Match Length I
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                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                       Searched:
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                                                                                         Run on:
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Sequence 12, Appl Sequence 179, App

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sequence 28, Application US/10092750
; Sequence 28, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFERENCE: 50036/050002
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO SEQ ED WINDOWS SEQ ID NOS: 268
; LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 127; DB 14;
Best Local Similarity 100.0%; Pred. No. 5.3e-12;
Matches 26; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/09098079; Patent No. US20020064773A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-092-750-28
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Gaps

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Sequence 1489, Application US/10408765A
; Sequence 1489, Application US/10408765A
; Publication No. US20040101874A1
; General InPORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glason, Bradford W.
APPLICANT: Glason, Dale E.
ITLE OF INVENTION: Dale E.
ITLE OF INVENTION: IDENTFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 66008465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; NUMBER OF SEQ ID NOS: 3077
; SOFTARER: FastSEQ for Windows Version 4.0
ch 88.2%; Score 112; DB 16; Length 603; 1 Similarity 96.0%; Pred. No. 3.4e-08; 24; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484 LYLKLTALAVTFLGLLTALDLNYLT 508
                                                                                                                                                                484 LYLKLTALAVTFLGLLTALDLNYLT 508
                                                                                                              2 LYLKLTALAVTFLGLLTALDLNYPT 26
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APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Boin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Conservative
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ORGANISM: Homo sapiens
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US-10-408-765A-2681
                        Best_Local_Similarity
Matches 24; Conserva
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Best Local Similarity
Matches 24; Conserva
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US-10-408-765A-2681
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LENGTH: 603
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LENGTH: 603
             Query Match
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  APPLICANT: Herrnstadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Glosh, Soumitra S.
APPLICANT: Clevenger, William
APPLICANT: Pahy, Boin F.
APPLICANT: Pahy, Boin F.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
TITLE OF INVENTION: EXTRAMITOCHONDDRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
SITREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-IU-408-765A-1487

Sequence 1487, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Tashy, Bing

APPLICANT: Tashy, Bing

APPLICANT: Tashon, Bradford W.

APPLICANT: Tashon, Bradford W.

APPLICANT: Tashon, Bradford W.

APPLICANT: Tashon, Bradford W.

APPLICANT: Glenn, Gary W.

APPLICANT: Glenn, Gary W.

APPLICANT: Warnock, Dale E.

ITILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

CURRENT APPLICATION NUMBER: US/10/408,765A

CURRENT APPLICATION NUMBER: US/10/408,765A

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077

SEQ ID NO 1487

ERGTH: 603

FURNIANDER: MINIMARY OF WINDOWS VERSION 4.0

SEQ ID NO 1487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-UN-1998
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: ROSSIMEN Ph.D., Stephen J.
REFERENCE/DOCKET NUMBER: 660088.416
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 LYLKLTALAVTFLGLLTALDLNYLT 508
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                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
TYPE: amino acids
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CRGANISM: Homo sapiens
US-10-408-765A-1487
                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
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Best Local Similarity
Matches 24; Conserv
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TOPOLOGY:
US-09-098-079-23
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APPLICANT: Zanay, Bolin D.
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Gibson, Glenn, Gary M.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DEBRIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT PPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFFWARE: FREESEQ for Windows Version 4.0
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Query Match

88.2%; Score 112; DB 16; Length 603;
Best Local Similarity 96.0%; Pred. No. 3.4e-08;
Matches 24; Conservative 0; Mismatches 1; Indels (
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Sequence 1488, Application US/10292798

Publication No. US2000235833A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ASMA, MAKING

APPLICANT: ARTHARA, YUTAKA,
TITLE OF INVENITON: GHANGSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFREENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT APPLICATION NUMBER: US/2-11-3
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR PILING DATE: 2001-12-18
PRIOR PILING DATE: 2001-6-18
NUMBER OF SEQ 1D NOS: 2070
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 148
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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                                               APPLICANT: STANDAY, MAKIKO
APPLICANT: SANI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ARIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
ITILE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
ITILE REFERENCE: 084335/015 25
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: UP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PARCEIL VET: 2.21
SEQ ID NO 1832
LENGTH: 299
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TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-186347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

41.7%; Score 53; DB 14;
Best Local Similarity 68.4%; Pred. No. 12;
Matches 13; Conservative 3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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; Publication No. US20040067499A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 68.4%;
Matches 13; Conservative
          Publication No. US20030143668A1
                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-017-161-1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-10-292-798-1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-10-343-650A-694
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                                                                                                                                   Sequence 71, Application US/10205219

Publication No. US20030138803A1

Publication No. US20030138803A1

GENERAL INFORMATION:

APPLICANT: Warner-Lambert Company

APPLICANT: Diaxon, Alistair

APPLICANT: Diaxon, Alistair

APPLICANT: Diaxon, Robert

TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

FILE REFERENCE: WL.A-01820

CURRENT FILING DATE: 2002-07-24

FRIOR APPLICATION NUMBER: GB 0118354.0

FRIOR APPLICATION NUMBER: GB 0118354.0

FRIOR FILING DATE: 2001-07-27

NUMBER OF SEQ ID NOS: 197

SEQ ID NO 71

LENGTH: 610
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APPLICANT ADLER, JON ELLIOT
ITILE OF INVENTION:
TITLE OF INVENTION T2R TASTE RECEPTORS AND GENES ENCODING SAME
TITLE OF INVENTION T2R TASTE 8009-04-05
CURRENT APPLICATION NUMBER: US/09/825,882
CURRENT PILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PLILORION NUMBER: 60/247,014
PRIOR FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 16
LENGTH: 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.7%; Score 53; DB 9; Length 299; 68.4%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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484 LYLKLTALAVTFLGLLTALDLNYLT 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 16, Application US/09825882 ; Patent No. US20020094551A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: NADH subunit 5 US-10-205-219-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LTALAVTFLGLLTALDLNY 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 68.4
Matches 13; Conservative
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US-09-825-882-16
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US-10-017-161-1832
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Gaps

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Gaps

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; SEQ ID NO 187
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-127-187
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ORGANISM: Oryza sativa
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LOCATION: (1)..(95)
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ORGANISM: Zea mays
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Sequence 187, Application US/10770127

Sequence 187, Application US/10770127

PUBLICATION OF USZO040214239A1

GENERAL INFORMATION:
APPLICANT: SERVANT, GUY
APPLICANT: OZECK, MARK
APPLICANT: BRUST, PAUL
APPLICANT: RIVENTION: FUNCTIONAL COUPLING OF TIRS AND T2RS BY GI PROTEIN
TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF TITLE OF INVENTION: AND T2R MODULATORS

FRICK APPLICATION UNMER: US/10/770,127

CURRENT APPLICATION NUMBER: 60/444,172

PRIOR APPLICATION NUMBER: 60/444,172

PRIOR APPLICATION NUMBER: 60/444,172

PRIOR APPLICATION NUMBER: 60/444,172

PRIOR APPLICATION NUMBER: 60/457,318

PRIOR FILING DATE: 2003-03-03

PRIOR FILING DATE: 2003-03-03

SOFTWARE: PATENTIN VETSION 3.2
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US-10-724-208-16
Sequence 16, Application US/10724208
Publication No. US2004020313A1
GENERAL INFORMATION:
INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/724,208
CURRENT APPLICATION NUMBER: 00/3-12-01
FILE REFERENCE: 2003-12-01
FRICE APPLICATION NUMBER: 60/195,532
FRICE APPLICATION NUMBER: 60/195,532
FRICE APPLICATION NUMBER: 60/247,014
FRICE FILING DATE: 2000-04-07
FRICE FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 16
LENGTH: 299
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                                                                                                                                                                                                                                                                                                       Score 53; DB 15; Length 299;
Pred. No. 12;
3; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SEGQ ID NO 694
LENGTH: 299
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LTALAVSRIGLLWALLLNW 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LTALAVTFLGLLTALDLNY 24
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48 LTALAVSRIGLEWALLLNW 66
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Best Local Similarity 68.4%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 68.4%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-10-724-208-16
                                                                                                                                                                                                                                     , ORGANISM: Homo sapiens
US-10-343-650A-694
                                                                                                                                                                                                                  TYPE: PRT
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Sequence 198410, Application US/10437963

Sequence 198410, Application No. US20040123343A1

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32315, Application US/10425115
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
REBERAL INFORMATION:
APPLICANT: Exoralic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPRENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 323215
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Pred. No. 56;
4; Mismatches 3; Indels
DB 17; Length 299;
                                                                                                    3; Indels
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, OTHER INFORMATION: Clone ID: PAT_MRT4530_94072C.1.pep
US-10-437-963-198410
Query Match
41.7%; Score 53; DB
Best Local Similarity 68.4%; Pred. No. 12;
Matches 13; Conservative 3; Mismatches
                                                                                                                                                                                                         6 LTALAVTFLGLLTALDLNY 24
                                                                                                                                                                                                                                                                         48 LTALAVSRIGLLWALLLNW 66
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700 YLQSSAMAVMFLGLLFAI 717
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Best Local Similarity 61.1%;
Matches 11; Conservative
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RESULT 15
10-424-599-241860
15-240-660, Application US/10424599
15-240-660-241860, Application US/10424599
15-240-660-241860, Application No. US20040031072A1
15-240-660-241860, Application No. US20040031072A1
15-240-241860, Application No. US2040031072A1
15-240-241860, Application No. US204003-24-28
15-240-241860, APPLICATION NUMBER: US/10/424,599
16-240-241860, USC 1285684
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                                                                                                                              Query Match 39.4%; Score 50; DB 17; Length 95; Best Local Similarity 52.4%; Pred. No. 9; Matches 11; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_60427C.1.pep
US-10-424-599-241860
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
. OTHER INFORMATION: Clone ID: MRT4577_57841C.1.pep
US-10-425-115-323215
                                                                                                                                                                                                                                 4 LKLTALAVTFLGLLTALDLNY 24
                                                                                                                                                                                                                                                               18 LLLSTLLTSGLGLLSALSINY 38
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|::|||:|||:|||
91 AISSTFLQVLTSLSISYP 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
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Search completed: November 11, 2004, 01:28:10 Job time : 28.9809 secs

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GenCore version 5.1.6
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Run on:

OM protein - protein search, using sw model

November 10, 2004, 12:29:32; Search time 5.79275 Seconds (without alignments) 431.857 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-092-750-28 127 1 TLYLKLTALAVTFLGLLTALDINYPT 26

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 200000000

PIR 79:* 1: pir1:* 2: pir2::* 3: pir3::* 4: pir4::* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	NADH2 dehydrogenas			NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas				NADH2 dehydrogenas	NADH2 dehydrogenas							NADH2 dehydrogenas		NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas					
SUMMARIES	CI	DNHC	T1414	B5915	T1402	T1419	T1414	T1184	T1150	82616		Н						T11464							T1149	S41	T1134	H		OXBO
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	Score	112	109	102	102	100	98	81	73.5	73.5	72.5	72	70	69.5	69	69	68	68	67	67	99	99	65.5	65.5	64	64	62	62	62	
	Result No.	1	8	m	4	ហ	Q	7	80	σ	10	11	12		14	15	16	17	18	19	20	21	22	23			26			

NADH2 dehydrogenas		-			NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH dehydrogenase	NADH2 dehydrogenas						
T11257	T11203	T11544	T14101	T14104	QXMS5M	T11774	T11438	C58889	T11190	T45560	T09867	T11516	T09957	C90627	C58893
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909	605	610	612	612	607	609	602	604	601	909	612	603	612	909	611
48.0	47.2	47.2	47.2	47.2	46.5	46.5	45.7	45.7	44.1	44.1	44.1	43.3	43.3	42.5	42.5
61	9	09	09	09	53	50	28	58		26	26	55	55	54	24

## ALIGNMENTS

	RESULT 1
	NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - human mitochondrion
	N'ALTERIACE names: NADH-Uniquinone Oxigoreductase chain 5
	C.bpc.s. ulrochouting objects (man- C.bpt.s. 22-Mav-1981 #sequence revision 23-Oct-1981 #text change 09-Unl-2004
	C;Accession: A00446; C00435; I80239
	R, Anderson, S.; Bankier, A.T.; Barrell, B.G.; de Bruijn, M.H.L.; Coulson, A.R.; Drouin,
,	Nature 290, 457-465, 1981
	A; Title: Sequence and organization of the human mitochondrial genome.
	A AREAErence number: AUU131; MU1D:811/3052; FM1D:713934 A Areaesion - A00446
	A: Molecule type: DNA
	A; Cross-references: UNIPROT: P03915; GB: J01415; NID: 91944628; PIDN: AAB58953.1; PID: 920523
	R.Brown, W.M.; Prager, E.M.; Wang, A.; Wilson, A.C.
	U. MOLL EVOL. 18, 252-253; 1982 3. Hitle, Withouthoughtial TMM segmentation of presentations
	alia illoae or
	A: Accession: C00435
	A; Molecule type: DNA
	A; Residues: 1-79 < BRO>
	A;Cross-references: GB:L00016; EMBL:V00658; NID:g337302
	A,Note: this ORF is not annotated in GenBank entry HUMMTTRPR, release 106
	R;Horai, S.; Hayasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
	Proc. Natl. Acad. Sci. U.S.A. 92, 532-536, 1995
	A/Title: Recent African origin of modern humans revealed by complete sequences of homino
	A;Reference number: I59384; MUID:95132634; PMID:7530363
	A;Accession: 180239
	A;Status: preliminary; translated from GB/EMBL/DDBU
	A; Molecule type: DNA
	A;Residues: 1-210,'P',212-256,'V',258-313,'V',315-455,'R',457-603 <hor></hor>
	A,Cross-references: DDBJ:D38112; NID:g644480; PIDN:BAA07297.1; PID:g704447
	A;Experimental source: African isolate SB17
	C.) GENETICS:
	A COUNTY OF THE PROPERTY OF TH
	A)CIOSS-TETETENCES: LDD:LIBSID; UMIN:DIBUOS
	A.Garome. mitochond-ion
	P. General Confession
	C.Superfamily: NADH dehydrogenase (ubjouinone) chain 5
	C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
	Querry March Bastat, Score LLZ; DB 1; Lengrn 603; Rest Loral Similarity 66.0%; Pred No. 2 ee.08;
	ā
	OV 2 INTERTAL DAVIDED CHILD INVOIT 26
	Db 484 LYLKITALAVTFLGLLTALDLNYLT 508
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C, accession: T14199
R; Hayasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
R; Hayasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
R; Horai, S.; Hayasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
R; Horai, S.; Hayasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
R; Horai, S.; Hayasaka, R.; Kondo, R.; Tsugane, K.; Takahata, N.
A; Reference number: 159384; MUID:95132634; PMID:7530363
A; Reference number: 159384; MUID:95132634; PMID:7530363
A; Reference number: 159384; MUID:95132634; PMID:7530363
A; Reference number: 150384; MUID:95132634; PMID:7530363
A; Reference number: 1503 A; Reference
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A,Genteic code: SGC1
C;Superfamily: NADH debydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
A;Title: Recent African origin of modern humans revealed by complete sequences of hominos. A;Reference number: IS9384; MUID:95132634; PMID:7530363
A;Accession: T14026
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Genome: mitochondrion
A,Genetic code: SGC1
C,Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C,Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NADRZ dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - chimpanzee mitochondrion C;Species: mitochondrion Pan troglodytes (chimpanzee) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ç,
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A;Residues: 1-603 <HOR>
A;Cross-references: UNIPROT:P03918; EMBL:D38115; PIDN:BAA07311.1
                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-603 <-HOL>
A;Cross-references: UNIPROT: P03917; EMBL: D38114; PIDN: BAA07306.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 102; DB 2; Length 603; Pred. No. 7.9e-07; 2; Mismatches 2; Indels
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Pred. No. 1.5e-06;
0; Mismatches 3; Indels
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Best Local Similarity 88.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 84.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: T14145
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                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
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T14199
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C)Accession: T14149
E/Accession: T14149
B/HOTAI, S.; Hayasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
Proc. Natl. Acad. Sci. U.S.A. 92, 532-536, 1995
A/Title: Recent African origin of modern humans revealed by complete sequences of hominc A/Accession: T14149
A/Accession: T14149
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Accession: Dreliminary; translated from GB/EMBL/DDBJ
A/Accession: D. Fellons
A/Accession: Breliminary; translated from GB/EMBL/DDBJ
A/Accession: Dreliminary; translated from GB/EMBL/DDBJ
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B59154
BA59154
BA5916
BA
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C;Accession: B99154
R;Xu, X.; Arnason, U.
Mol. Biol. Evol. 13, 691-698, 1996
A;Title: A complete sequence of the mitochondrial genome of the Western lowland gorilla.
A;Reference number: 217269; MUID:96212991; PMID:8676744
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A;Molecule type: DNA
A;Residues: 1-603 <XUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfainly: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                               chimpanzee mitochondrion
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A)Note: submitted to GenBank, November 1995
A)Note: this translation is not annotated in GenBank entry GGMITG, release 114.0
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                                                                                                                                                                                         NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - pygmy chimpanzee mi
C;Species: mitochondrion Pan paniscus (pygmy chimpanzee, bonobo)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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Pred. No. 7.8e-08;
1; Mismatches 1;
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Best Local Similarity 92.0%;
Matches 23; Conservative
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A;Genome: mitochondrion
A;Gentetic code: SGC1
C;Superfamily: NADH debydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
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A,Experimental source: female adult; isolate FCA-65; lymphocyte; blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-raferences: UNIPROT: Q00542; EMBL: X63726; NID: g13431; PIDN: CAA45267.1; PID: g13442
C; Genetics:
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C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Nabla dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - harbor seal mitochondrion Nabla dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - harbor seal mitochondrion Phoca vitulina (harbor seal)
C;Species: mitochondrion Phoca vitulina (harbor seal)
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S2616.
G;Arascon, U.; Johnsson, E.
J. Mol. Evol. 34, 493-505, 1992
A;Title: The complete mitochondrial DNA sequence of the harbor seal, Phoca vitulina.
A;Title: momplete mitochondrial DNA sequence of the harbor seal, Phoca vitulina.
A;Reference number: S26151; MUID:92277666; PMID:1593642
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - pig mitochondrion
C;Species: mitochondrion Sus scrofa domestica (domestic pig)
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    Length 606;
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    DB 2;
.0093;
les 3;
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Pred. No. 0.0094;
3; Mismatches 4;
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                                                                                                                                                                                                                                  485 YLKMTALAVITLGFILALBLNLTSQGLKFNYPS 517
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         Score 73.5; D
Pred. No. 0.00
4; Mismatches
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         Query Match 57.9%;
Best Local Similarity 51.5%;
Matches 17; Conservative
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ilarity 51.5%;
Conservative
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
Matches 17; Conserv
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A; Molecule type: DNA
A; Residues: 1-609 <ARN>
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A; Residues: 1-606 <L
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C.Accession: Tile43, Anot449
R.Arnason, U.; Gullberg, A.; Xu, X.
Recence number: 21733
A.Accession: Tile43
A.Accession: Anot49
A.Ac
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - dog mitochondrion

C,Species: mitochondrion Canis luque familiaris (dog)

C,Date: 16-Uul-1999 #sequence_revision 16-Uul-1999 #text_change 03-Uun-2002

C,Accession: T11503

R,Kim, K.S.; Lee, S.E.; Jeong, H.W.; Ha, J.H.

Mol. Phylogenet. Evol. 10, 210-220, 1998

A,Fitle: The complete nucleotide sequence of the domestic dog (Canis familiaris) mitochc

A,Recession: T11503

A,Residues: Lefo «KIM»

A,Residues: Lefo «KIM»

A,Residues: Lefo «KIM»

A,Genetics:
A,Genemics: Mitochondrion

A,Genemic code: SGC1

A,Genemic code: SGC1

A,Genemic witochondrion

A,Genemic we NDS

C,Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C,Keywords: membrane-associated complex, mitochondrion, NAD; oxidative phosphorylation,
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         Length 603,
Query Match 67.7%; Score 86; DB 2; Length 603
Best Local Similarity 78.3%; Pred. No. 0.00015;
Matches 18; Conservative 0; Mismatches 5; Indels
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Pred. No. 0.00079;
3; Mismatches 5; Indels
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                                                                                                                                                                               2 LYLKLTALAVTFLGLLTALDLNY
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Best Local Similarity 68.0%;
Matches 17; Conservative
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - nine-banded armadillo mitochondrii C; Species: mitochondrion Dasypus novemcinctus (nine-banded armadillo) (C; Date: 16-U1-1999 #sequence_revision 16-U1-1999 #text_change 09-U1-2004 (C; Accession: T11451 (S; Armason, U.; Gullberg, A.; Janke, A. Mol. Biol. Evol. 14, 762-768, 1997 (A; Armason, U.; Gullberg, A.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; (
                                                                                    domestic sheep (Ovis aries) and c
                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:078756; EMBL:AF010406; NID:g3445513; PID:g3366632; PIDN:AAD1(
A;Experimental source: strain Merinolandschaf; liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-601 <ARN>
A;Cross-references: UNIPROT:021335; EMBL:Y11832; NID:92252500; PIDN:CAA72521.1; PID:92252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyaccession: T11867
TX, X.; Arnason, U.
Gene 148, 357-362, 1994
A;Title: The complete mitochondrial DNA sequence of the horse, Equus caballus: Extensive A;Title: The complete MID:95047450; PMID:7958969
A;Acedession: T11867
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-604 <XUX>
A; Residues: 1-604 <XUX>
C; Genetics: UNIPROT: P48656; EMBL: X79547; NID: 9577571; PID: 9577582; PIDN: CAAS6089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: ND5
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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R;Hiendleder, S.; Lewalski, H.; Wassmuth, R.; Janke, A. J. Mol. Evol. 47, 441-448, 1998
A;Title: The complete mitochondrial DNA sequence of the A;Reference number: Z17245; MUID:98440761; PMID:9767689
A;Accession: T11060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-606 <HIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 69.5; DB 2
Pred. No. 0.035;
5; Mismatches
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Pred. No. 0.041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 54.7%;
Local Similarity 45.5%;
es 15; Conservative
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Best Local Similarity 59.1%;
Matches 13; Conservative
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A,Genome: mitochondrion
A,Genetic code: SGC1
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Best Loca
Matches
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10982; T11880
E;Lin, C.S.; Liu, C.Y.; Sun, Y.L.; Chang, L.C.; Cheng, I.C.; Yang, P.C.; Mao, S.J.T.; Hu submitted to the EMBL Data Library, November 1997
A;Description: Complete nucleotide sequence of the porcine mitochondrial genome.
A;Reference number: Z17237
                                                                                                                                                                                                                                                                                     ;Status: preliminary; translated from GB/EMBL/DDBJ
;Molecule type: DNA
;Residues: 1-606 <LIN>
;Cross-references: UNIPROT:Q9TDR1; EMBL:AF034253; NID:g4958951; PID:g4958962; PIDN:AAD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: T11399
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-603 <REY>
A,Cross-references: UNIPROT:O63908; EMBL:AJ001562; NID:G3127895; PIDN:CAA04840.1; PID:g3
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A;Genetic code: SGCI
Styperfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - fat dormouse mitochondrion C;Species: mitochondrion Myoxus glis (fat dormouse)
C;Species: mitochondrion Myoxus glis (fat dormouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: Til399
R;Reyes, A.; Pesole, G.; Saccone, C.
MyTitle: Complete mitochondrial DNA sequence of the fat dormouse, Glis glis: further A;Reference number: Z17267; MUID:98242079; PMID:9580978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NADH2 dehydrogenase (ubiquinone) (EC 1.5.5.3) chain 5 - sheep mitochondrion C;Species: mitochondrion Ovis orientalis aries, Ovis ammon aries (domestic sheep) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T11060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Ursing, B.M. submitted to the EMBL Data Library, February 1999 A;Description: The complete mitochondrial DNA sequence of the pig (Sus scrofa). A;Reference number: Z17370 A;Reference number: Z17370
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Residues: 1-12,'T',14-121,'L',123-590,'S',592-606 <URS>
Cross-references: EMBL:AJ002189; PIDN:CAA05241.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 0.029;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72; DB
Pred. No. 0.01
5; Mismatches
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Best Local Similarity 66.7%;
Matches. 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 56.0%;
Matches 14; Conservative
                                                                                                                                                                                                                                                            Accession: T10982
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T11060
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A;Genome: mitochondrion C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Ouery Match
Best Local Similarity 62.5%; Pred. No. 0.041;
Matches 15; Conservative 3; Mismatches 6; Indels

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0; Gaps

ઠે g Search completed: November 10, 2004, 13:40:37 Job time : 6.79275 secs

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November 10, 2004, 12:27:34; Search time 31.7478 Seconds (without alignments) 471.205 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                               OM protein - protein search, using sw model
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Run on:

US-10-092-750-28 127 1 TLYLKLTALAVTFLGLLTALDLNYPT 26 Title: Perfect score: Sequence:

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 Total number of hits satisfying chosen parameters:

1825181 seqs, 575374646 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45.summaries UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		homod		ø		homo sapien		homo sapien								homo sapien			homo sapien	homo sapien	homo sapien									homo sapien		homo sapien
	Descrip	Aat38537							Qernjo h								Q6vi79 h			Qevixe h				Q7y6h2 h						~	m	
SUMMARIES	Ω	AAT38537	AAT38538	NUSM HUMAN	Q6PZ <u>3</u> 5	Q6RMF4	Q6RMK4	QGRMMS	QGRNJO	Q6RNL1	QGRPF2	Q6RQ14	QERRRO	Q6RS00	Q6RS27	Q6VHD5	Q6VI79	QEVIDS	QEVIF3	Q6VIX6	Q6VIZ4	Q6VKL7	Q6WQ97	Q7Y6H2	Q7Y622	Q7Y7F0	Q7Y823	Q7YCC4	Q7YCD7	7YCD	7.	O7YCF6
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RESULT 2
AAT36538
ID AAT36538
ID AAT36538
ID O1-JUN-2004 (TrEMBLrel. 27, Created)
DT O1-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT O1-JUN-2004 (TrEMBLrel. 27, Last annotation update)
OS Momon appiens (Human).
OS Mitochondarion.
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NOBI TaxID=9606;
NN [1]
RP SEQUENCE FROM N.A.
RC STRAINS-22807936;
RX MEDLINE-22807936;
RX MEDLINE-22807936;
RX MEDLINE-22807936;
RX MEDLINE-22807936;
RX MEDLINE-22807936;
RA KONG Q.-P., Yao Y.-G., Sun C., Bandelt H.-J., Zhang Y.-P.;

[1] -SEQUENCE FROM N.A. STRAIN=QD8147; MEDIAINE-22807936; PubMed=12870132; Kong Q.-P., Yao Y.-G., Sun C., Bandelt H.-J., Zhu C.-L., Zhang Y.-P.;

sapien sapien sapien sapien sapien sapien sapien sapien sapien
hongo
077 090 077 090 070 070 070 070 070 070 070 070 070
Q7YCG0 Q7YCG8 Q7YCH1 Q7YED0 Q7YED0 Q7YEF0 Q7YEF2 Q7YEF2 Q7YEF3 Q7YEF3 Q7YEF3 Q7YEF3
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## ALIGNMENTS

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Matches

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Ingman M., Gyllensten U.; "Mitochondrial genome variation and evolutionary history of Australian and new guinean aborigines."; Genome Res. 13:1600-1606(2003).
                                                                                                                  SEQUENCE FROM N.A.
PubMed=14766490; DOI=10.1007/s00414-004-0427-6;
Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T., Irwin J.A., Parsons T.J.;
Irwin J.A., Parsons T.J.;
Single mucleocitde polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               identification of PROTEIN.
MEDLINE=85188293; PubMed=3921850;
Chomyn A., Mariottini P., Cleeter M.W.J., Ragan C.I., Matsuno-Yagi A.,
Hatefi Y., Doolittle R.F., Attandi G.;
"Six unidentified reading frames of human mitochondrial DNA encode
components of the respiratory-chain NaDH dehydrogenase.";
Nature 314:592-597(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome.";

Nucleic Acids Res. 26:967-973(1998).

Nucleic Acids Res. 26:967-973(1998).

-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

-!- SUBCELLULAR LOCATION: Integral membrane protein, mitochondrial inner membrane (Probable).

-!- DISEASE: Defects in MYNDS are a cause of Leber's hereditary optic neuropathy (LHON) [MIM:535000]; also known as Leber's optic atrophy. LHON is a maternally inherited disease resulting in acute bilateral blindhess due to retinal degeneration predominantly in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrial DNA complex I and III mutations associated with Leber's
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MEDLINE-2908084; PubMed=1757091;
MATULINE-2908084; PubMed=1757091;
MATULINE-2908084; PubMed=1757091;
Utthanaphol P., Byrne E.;
"Normal variates of human mitochondrial DNA and translation products:
"Normal variates of a reference data base.";
Hum. Genet. 88:139-145(1991).
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Rieder M.G., Taylor S.L., Tobe V.O., Nickerson D.A.;
"Autometing the identification of DNA variations using quality-based
fluorescence re-sequencing: analysis of the human mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS SER-17; SER-95; PRO-99; ASP-146; VAL-160; SER-165; SER-304;
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MEDLINE=91144615; PubMed=1900003;
Johns D.R., Berman J.;
"Alternative, simultaneous complex I mitochondrial DNA mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McCullough D.A., Poulton J., become Leber hereditary optic
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MEDLINE=22120513; PubMed=1732158;
Brown M.D., Voljavec A.S., Lott M.T., Torroni A., Yang C.C.,
Wallace D.C.;
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                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-79 FROM N.A. MEDLINE-82242101; PubMed-6284948; MEDLINE-82242101; PubMed-6284948; Brown W.M., Farger E.M., Wang A., Wilson A.C.; Mitcochondrial DNA sequences of primates: tempo and mode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leber's hereditary optic neuropathy.";
Biochem. Biophys. Res. Commun. 174:1324-1330(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT LHON GLU-465.
MEDLINE=94027064; PubMed=8213825;
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Genetics 130:163-173(1992).
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PubMed-12949126; DOI=10.1093/molbev/msg230;
Moilanen J.S., Finnila S., Majamaa.K.;
"Lineage-specific selection in human mtDNA: lack of polymorphisms in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Horai S., Hayasaka K., Kondo R., Tsugane K., Takahata N.; "Recent African origin of modern humans revealed by complete sequences of hominoid mitochondrial DNAs."; Proc. Natl. Acad. Sci. U.S.NA. 92:532-536(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDUINE=21012010; PubMed=11130070; DOI=10.1038/35047064;
Ingman M., Kaessmann H., Paabo S., Gyllensten U.;
"Mitochondrial genome variation and the origin of modern humans.";
Nature 408:708-713(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
  "Phylogeny of east Asian mitochondrial DNA lineages inferred from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=81173052; PubMed=7219534;
Anderson S., Bankier A.T., Barrell B.G., de Bruijn M.H.L.,
Coulson A.R., Drouin J., Eperon I.C., Nierlich D.P., Roe B.A.,
Sanger F., Schreier P.H., Smith A.J.H., Staden R., Young I.G.;
"Sequence and organization of the human mitochondrial genome.";
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                                                                                                                                                                   Length 601;
                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=22723755; PubMed=12840039; DOI=10.1101/gr.686603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kogelnik A., Brown M.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                             601 AA; 66837 MW; 6CA20C0C96FBD3B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    MUSM HUMAN STANDARD; PRT; 603 AM.
P03915; C34773; CBWCY3;
21-JUL-1986 (Rell. 01, Caeted)
30-MAY-2000 (Rell. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
NADH-ubiquinone oxidoxeductase chain 5 (EC 1.6.5.3).
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96.0%; Pred. No. 2...
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                                                                                                                                                                                                                                                                                           482 LYLKUTALAVTFLGLLTALDLNYLT 506
                                                                                                                                                                                                                                                               2 LYLKLTALAVTFLGLLTALDLNYPT 26
                      complete sequences.";
Am. J. Hum. Genet. 73:671-676(2003).
EMBL; AY255180; AAT38538.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95132634; PubMed=7530363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=MTNĎ5; Synonyms=ND5;
Homo sapiens (Human).
                                                                                                                                                                                                                24; Conservative
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                                                                                           Mitochondrion
SEQUENCE 60
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RESULT OF SECOND SECOND

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00-10-037-120-0T-8D
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Length 603

Query Match 88.2%; Score 112; DB 1; Length 60 Best Local Similarity 96.0%; Pred. No. 2.9e-07; Matches 24; Conservative 0; Mismatches 1; Indels

484 LYLKLTALAVTFLGLLTALDLNYLT 508

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2 LYLKLTALAVTFLGLLTALDLNYPT 26

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young men. Cardiac conduction defects and neurological defects have also been described, resulting in optic nerve degeneration and cardiac dysrbythmia.

SIMILARITY: Belongs to the complex I subunit 5 family.
                                                                                                                                                                                                                                                                                                EMBL, J01415, AABS8953.1, --
EMBL, WO0662, CAA44036.1, --
EMBL, AF465942, AAN14556.1, --
EMBL, AF485942, AAN14556.1, --
EMBL, AY339401, AAP89005.1, --
EMBL, AY339404, AAP89005.1, --
EMBL, AY339404, AAP89005.1, --
EMBL, AY339406, AAP89008.1, --
EMBL, AY339406, AAP89111.1, --
EMBL, AY339406, AAP89111.1, --
EMBL, AY339409, AAP89113.1, --
EMBL, AY3394109, AAP89113.1, --
EMBL, AY3394109, AAP89113.1, --
EMBL, AY3394109, AAP89113.1, --
EMBL, AY339410, AAP89113.1, --
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AY339457;
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AAP89761.1;

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                                                                                  Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 96.0%; Pred. No. 2.9e-07;
Matches 24; Conservative 0; Mismatches 1; Indels
                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 5.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 5.
                  603 AA
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                  PRT;
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                  PRELIMINARY;
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                                                                          Homo sapiens (Human).
                                                                                                          NCBI_TaxID=9606;
                                                                  Name=ND5
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QGRMF4;
                 Q6PZ35
Q6PZ35;
RESULT 4
Q6PZ35
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QERMF4
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                           ch 88.2%; Score 112; DB 2; Length 603; 1 Similarity 96.0%; Pred. No. 2.9e-07; 24; Conservative 0; Mismatches 1; Indels
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PERNTS, PRO1434; NADHDHGNASES.
PRINTS, PRO1435; NPOXDRDTARSES.
TIGRPAMS, TIGRNAS1974; NDH_I_L; I.
Mitchansion; NDS) Oxidoreductase; Ubiquinone.
SEQUENCE 603 Aa; 67014 MW; 18A0623B7A04162A CRC64;
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Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 603 AA; 67012 MW; 567A22F7E813C766 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 5.
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InterPro; IPR003945; NADHUD oxred5.
InterPro; IPR0017916; Oxidored_q1.
InterPro; IPR0017516; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.
Pfam; PF006455; NRDH5_C; 1.
Pfam; PF00061; Oxidored_q1, 1.
Pfam; PF001434; NADHDHGNASE5.
PRINTS; PR01434; NADHDHGNASE5.
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Matches 24; Conservative
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Mitochondrion.
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SEQUENCE FROM N.A.
PubMed=14760490;
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Best Local 8
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ID QERNJO
AC QERNJO;
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QERMMS
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SEQUENCE FROM N.A.

Pubmed-14760490;

Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

Pubmed-14760490;

Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

Interpose the power of forensic testing in Caucasians.";

Interpose the power of foren
                                                                                                                                                           Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T., Irwin J.A., Parsons T.J.;
Irwin J.A., Parsons T.J.;
"Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians.";
Int. J. Legal Wed. 0:0-0(2004).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SUBCELDULAR LOCATION: Integral membrane protein, mitochondrial
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Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.9e-07;
0; Mismatches 1; Indels
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Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 603 AA; 67010 MW; 7561BE3A77C9023F CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Name=ND5;
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Best Local Similarity 96.0%;
Matches 24; Conservative (
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                       NCBI_TaxID=9606;
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AC 06 RM
AC 06 RM
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Gaps

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We Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T., A. Irwin J.A., Parsons T.J., Parsons T.J
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PubMed=1476490;

PubMed=1476490;

Coble M.D.; Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

Irwin J.A., Parsons T.J.;

"Single nucleotide polymorphisms over the entire mtDNA genome that

"Single nucleotide polymorphisms over the entire mtDNA genome that

"Single nucleotide polymorphisms over the entire mtDNA genome that

"Single nucleotide polymorphisms over the entire mtDNA genome that

"Single nucleotide polymorphisms over the entire mtDNA genome that

"Int. J. Legal Med. 0:0-0(2004).

-I- CATALYTIC ACTIVITY: NaDH + ubiquinone = NAD(+) + ubiquinol.

-I- SUBCELLUIAR LOCATION: Integral membrane protein, mitochondrial

inner membrane (By similarity).

-I- SIMILARITY: Belongs to the complex I subunit 5 family.
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                                                                                                                                                             Name=NDS;
Homo sapions (Human).
Homo sapions (Human).
Homo sapions (Human).
Homo sapions (Human).
Homondation.
Hoteacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 603 AA; 67068 MW; 19EC35C76A491631 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGRNL1;
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 5.
05-JUL-2004 (TrEMBirel. 27, Created)
05-JUL-2004 (TrEMBirel. 27, Last sequence update)
05-JUL-2004 (TrEMBirel. 27, Last annotation update)
NADH dehydrogenase subunit 5.
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06RNL1
AC 06RNL
AC 06RNL
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Coble M.D., Just R.S., C'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
R. Pubbed-14760490;
R. Coble M.D., Just R.S., C'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
R. Irwin J.A., Parsons T.J.,
R. Irwin J.A., Parsons T.J.,
R. Increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
C. !- SUMCELLUTAR LOCATION: Integral membrane protein, mitochondrial
CC. !- SUMCELLUTAR LOCATION: Integral membrane protein, mitochondrial
CC. !- SIMILARITY: Belongs to the complex I subunit 5 family.
C. !- SIMILARITY: Belongs to the complex I subunit 5 family.
CO. GO:005739; C:mitochondrion; IEA.
REMEL, AX495195; AAR93871.1; -.
REMEL, AX495195; NADHE C.:
RICEPERO; IPRO1934; NADHE C.:
RICEPERO; IPRO1934; NADHE C.:
RICEPERO; IPRO1934; NADHE C.:
REMEL, PRO1934; NADHENASES.
RINTS; PRO1435; NADHENASES.
REMINTS; REMINTS; PRO1435; NADHENASES.
REMINTS; REMIN
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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EMBL, AY495224; AAR94248.1; -.. GO; GO:0005739; C:mitochondrion; IBA.
InterPro; IPR010934; NADHD_ Oxreds.
InterPro; IPR003945; NADHD_ Oxreds.
InterPro; IPR003916; NADHD_ Oxreds.
InterPro; IPR001709; Oxidored_q1.
InterPro; IRR001709; Oxidored_q1.
InterPro; IRR001709; Oxidored_q1.
InterPro; IRR00361; Oxidored_q1.
IN Pfam; PP06361; Oxidored_q1.
IN Pfam; PP06361; Oxidored_q1.
IN PRINTS; PR01434; NADHDHGNASES.
ITGRFAMS; TIGR01974; NDH I L; 1.
ITGRFAMS; TIGR01974; NDH I L; 1.
IN MICOChondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 603 AA; 67026 MW; 14878214A01813A2 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 5.
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484 LYLKLTALAVTFLGLLTALDLNYLT 508
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PEm., PP00361; Oxidozed_q1, 1.
PEdm., PP00662; Oxidozed_q1, N. 1.
PRINTS; PR01434; NADHDEGNASES.
PRINTS; PR01435; NPOXDEDTASES.
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Homo sapiens (Human).
Mitochondrion.
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PubMed=14760490;
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QERSOO;
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Trwin J.A., Parsons T.J.;

Trwin J.A., Just B.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T., C.T., Lagal Med. 0:0-0(2004).

The case the power of forensic testing in Caucasians.";

Int. J. Legal Med. 0:0-0(2004).

L. CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

C. I. CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

C. I. SIBCLIGITARITY: Belongs to the complex I subunit S family.

EMBL: AY495153; ARAB3325-1; -.

REBL: AY495153; ARAB3325-1; -.

REBL: AY4901934; NADHS C.

InterPro; IPR001934; NADHS C.

RINTERPRO; IPR001936; NADHUL CANTEGS.

RINTERPO; IPR001936; NADHUL CANTEGS.

RINTERPRO; IPR001936; NADHUL CANTEGS.
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PubMed=14760490;
Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
Irwin J.A., Parsons T.J.;
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Homo sapiens (Human).

Buktochondricon.

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Pred. No. 2.9e-07;
0; Mismatches 1; Indels
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 5.
                                                                                                                                                                                                           603 AA
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    484 LYLKLTALAVTFLGLLTALDLNYLT 508
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                                                                                                                                                                                                                PRT;
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96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
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SEQUENCE FROM N.A.
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26RRR
AC 26RRR
AC 26RRR
AC 26RRR
DT 05-JU
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CS HOMO
CG MARMAR
OC MARMAR
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CO MARMAR

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Q6RQI4
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Gaps
"Single nuclectide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians."; Int. J. Legal Med. 0:0-0(2004).
-!- CATLLYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SUBCELLULAR LOCATION: Integral membrane protein, mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                             inner membrane (By smilarity).

1. SIMILARITY: Belongs to the complex I subunit 5 family.

R GO; GO:0005739; Cimitochondrion; IEA.

R InterPro: IPR01034; NADH5_C.

R InterPro: IPR030345; NADH5_C.

R InterPro: IPR030345; NADH5_C.

R InterPro: IPR031516; Oxidored_q1.

R InterPro: IPR031516; Oxidored_q1.

R Efam; PF06455; NADH5 C:

R Ffam; PF06465; NADH5 C:

R FRINTS; PR0435; NPOXDEASE5.

R TIGRAMS; TIGR01974; NH I.L. 1.

R Mitcchondrion; NA); Oxidoreductase; Ubiquinone.

SEQUENCE 603 AA; 67038 MW; E1A9339B22D187A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 112; DB 2; Length 603;
Pred. No. 2.9e-07;
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-1- SIMILARITY: Belongs to the complex I subunit 5 family.

Ball, Avg 195096; ARP25841.

GO; GO:0005739; C:mitochondrion; iEA.

InterPro; IPR010934; NADH5 C.

InterPro; IPR003945; NADH5 oxred5.

InterPro; IPR003916; NADH0 oxred5.

InterPro; IPR001750; Oxidored_q1.

InterPro; IPR0017516; Oxidored_q1.
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Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 603 AA; 67040 MW; IFD76557DCCE612A CRC64;
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 5.
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96.0%; Pred. No. 2...
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Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                          SEQUENCE FROM N.A.
Mammalia, Euther:
NCBI_TaxID=9606;
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22 SEQUENCE FROM N.A.

23 PubMed=14760490;

24 CADDLE M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

25 R. Train J.A., Parsons T.J.;

26 Irwin J.A., Parsons T.J.;

27 Increase the power of forensic testing in Caucasians.";

27 Increase the power of forensic testing in Caucasians.";

28 Int. J. Legal Med. 0.0-0(2004).

27 Increase the power of forensic testing in Caucasians.";

28 Int. J. Legal Med. 0.0-0(2004).

29 Int. J. Legal Med. 0.0-0(2004).

20 Int. J. Legal Med. 0.0-0(2004).

20 Int. J. Legal Med. 0.0-0(2004).

20 Int. J. Legal Med. 0.0-0(2004).

21 Int. J. Legal Med. 0.0-0(2004).

22 Int. J. Legal Med. 0.0-0(2004).

23 Int. J. Legal Med. 0.0-0(2004).

24 M.495093; AAR92545.1; -..

26 InterPro; IPR001934; NADH5 C.

27 Int. J. Legal Med. 0.0-0(2004).

28 InterPro; IPR001916; Oxidored q1.

29 Refan; PF00645; Oxidored q1; 1.

20 Refan; PF00784; NADHDHGNASES.

20 RENTYS; PR01434; NADHDHGNASES.

20 Refan; PF00784; Oxidored q1; 1.

20 Refan; PF00784; Oxidored q1; 1.

21 Refan; PF00784; Oxidored q1; 1.

22 Refan; PF00784; Oxidored q1; 1.

23 Refan; PF00784; Oxidored q1; 1.

24 Refan; PF00784; Oxidored q1; 1.

25 Refan; PF00784; Oxidored q1; 1.

26 Refan; PF00784; Oxidored q1; 1.

27 Refan; PF00784; Oxidored q1; 1.

28 Refan; PF00784; Oxidored q1; 1.

28 Refan; PF00784; Oxidored q1; 1.

29 Refan; PF00784; Oxidored q1; 1.

20 Refan; PF00784; Oxidored q1; 1.
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Mitochondrion.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mitochondrion.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                      Query Match 88.2%; Score 112; DB 2; Length 603; Best Local Similarity 96.0%; Pred. No. 2.9e-07; Matches 24; Conservative 0; Mismatches 1; Indels
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96.0%; Pred. No. 2.9e-07;
ive 0; Mismatches 1; Indels
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Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 603 AA; 67038 MW; 032A41FA9D6E18DA CRC64;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 5.
                                                                                                                                                                                                                                                                                                          603 AA
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                                                                                                                         2 LYLKLTALAVTFIGLITALDINYPT 26
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Name=ND5;
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Best Local Similarity 96.0%
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05-JUL-2004
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QGVHD5
ID QGVHD
AC QGVHD
DT 05-JU
DT 05-JU
DT NADH (GN Name=)
OS HOMO
OG Mitcol
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Q6RS27
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EXURENCE FROM N.A.

EXPLEMENTS FROM N.A.

EXPLEMENTS FROM N.A.

EXPLEMENTS FROM N.A.

Invin J.A., Parsons T.J.; Letmanyi I.H., Peterson C.T.,

Irwin J.A., Parsons T.J.; Letmanyi I.H., Peterson C.T.,

Irwin J.A., Parsons T.J.; Letmanyi I.H., Peterson C.T.,

Increase the power of forensic testing in Caucasians.";

Int. J. Legal Med. 0:0-0(2004)

Int. SUBCILLULAR IX. Palongs to the complex I subunit 5 family.

EMBL; AV495231; AAR943351; --

EMBL; AV495231; AAR943521; --

EMBL; AV495233; AAR94391:]; --

EMBL; AV495233; AAR94406:1; --

EMBL; AV495234; AAR94406:1; --

EMBL; AV495236; AAR94406:1; --

EMBL; AV495236; AAR94406:1; --

EMBL; AV495239; AAR94400:1; --

EMBL; AV495239; AAR9400:1; --

EMBL; AV495200; AAR9400:1; --

EMBL; AV495200; AAR9
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                                                                                                                                                                                                                                                                            PubMed=12949126;
Mollanen J.S., Finnila S., Majamaa K.;
Mollanen J.S., Finnila S., Majamaa K.;
"Lineage-specific selection in human mtDNA: lack of polymorphisms in
segment of MTNDS gene in haplogroup J.";
Mol. Biol. Evol. 20:2132-2142(2003).
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MEDLINE=21313109; PubMed=11349229;
Finnila S., Lehtonnen M.S., Majamaa K.;
"Phylogenetic network for Buropean mtDNA.";
Am. J. Hum. Genet. 68:1475-1484(2001).
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Best Local Similarity 96.0%;
Matches 24; Conservative
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FEATURE:
NAMM/KEY: misc feature
LOCATION: (B) LOCATION 1...396
SEQUENCE DESCRIPTION: SEQ ID NO: 5033:
US-09-107-532A-5033
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5033, Ap Sequence 4633, Ap Sequence 4633, Ap Sequence 3136, A Sequence 21346, A Sequence 21346, Ap Sequence 4, Appli Sequence 15, Appli Sequence 5, Appli Sequence 5, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 14, Appli Sequence 11, Appli Appli Sequence 11, Appli Appli
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191.991 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                      US-10-092-750-29
229
1 AGVFSAEPSPFPQTRRSMVF.....REVGDEFRSRHLNSTDDADE
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/cgn2_6/ptodata1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata1/liaa/6A_COMB.pep:*
/cgn2_6/ptodata1/liaa/6A_COMB.pep:*
/cgn2_6/ptodata1/liaa/6B_COMB.pep:*
/cgn2_6/ptodata1/liaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata1/liaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata1/liaa/backfiles1.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-107-532A-5033

US-09-252-991A-31650

US-09-252-991A-3150

US-09-252-991A-32150

US-09-252-991A-21346

US-09-134-000C-4666

US-09-134-000C-4666

US-09-134-000C-4666

US-09-134-000C-4666

US-09-134-000C-4666

US-09-134-00C-4666

US-09-134-00C-4666

US-09-134-00C-4666

US-09-134-00C-4666

US-09-134-134-14

US-08-10C-636-10

US-08-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                          November 10, 2004, 12:32:37
                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seg length: 200000000
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                             Run on:
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No.
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Sequence 1112, Ap Sequence 11795, A Sequence 6, Appli Sequence 247, Appli Sequence 2477, Ap Sequence 10819, A Sequence 10, Appl Sequence 88, Appl Sequence 88, Appl Sequence 11, Appli Sequence 2, Appli Sequence 2, Appli Sequence 57, Appli Sequence 56, Appli Sequence 56, Appli		ush ID SEQUENCES RELATING TO DIAGNOSTICS AND THERAPEUTI ON
310 4 US-09-710-279-1312 370 4 US-09-489-039A-11795 394 3 US-09-480-039A-11795 394 4 US-09-218-197-2 394 4 US-09-218-197-2 414 3 US-09-218-197-2 414 3 US-09-248-0105-5377 415 4 US-09-543-681A-7181 27 2 US-08-718-108 27 2 US-08-718-11 27 2 US-08-924-695A-88 27 2 US-08-924-695A-88 27 2 US-08-924-695A-88 27 3 US-09-255-991A-31350 27 3 US-09-255-991A-31350 275 3 US-09-255-991A-31350 275 3 US-09-255-991A-31350 275 3 US-09-255-991A-31350 275 3 US-09-255-991A-31350 275 3 US-09-328-325-573 289 2 US-08-733-505A-55	ALIGNMENTS	US/09107532A  UCCELTE-Stamm and David Busi NUCLEIC ACID AND AMINO ACID ENTEROCOCCUS FAECIUM FOR DII 330 355: WHE THERAPEUTICS CORPORATION (Ver Street 18etts  DATA: BER: US/09/107,532A 174: BER: 60/085,598 174: BER: 60/081571 11,9 2, 1997 MAY 1998 BER: 40,489 FFORMATION: 1,893-5007 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-803: 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-8277 1,93-83-838
51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51.5		NO. 6 8 122A NO. 6 8 122A NO. 6 8 12 11 11 11 11 11 11 11 11 11 11 11 11
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WS-09-252-991A-32150

WS-09-252-991A-32150

Sequence 32150, Application US/09252991A

Sequence 32150, Application US/09252991A

Sequence 32150, Application US/09252991A

Sequence 32150, Application US/09252991A

Tarten Vo. 6551710S

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE NEPRENCE: 10716-136

FILE REPERENCE: 10716-136

PRIOR APPLICATION NUMBER: US/09/252,991A

PRIOR PRIING DATE: 1998-02-18

PRIOR PRIING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

WUMBER OF SEQ ID NOS: 33142

LENGTH: 506
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Sequence 21346, Application US/09252991A
Sequence 21346, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.7%; Score 56.5; DB 4; Length 376; llarity 35.7%; Pred. No. 9.2; Conservative 6; Mismatches 18. Thanh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.7%; Score 56.5; DB 4; Length 506; 33.3%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 PLGVPETEAALVFLRHRREQGRDQPRRTGGGGDQHRAAH 202
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Mismatches
                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEPAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 4633:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHATICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                              )

NAME/KEY: misc_feature
;
LOCATION: (B) LOCATION 1...376
;
US-09-107-532A-4633
GTC-012
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32150
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Matches 15; Conserva
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Sequence 31650, Application US/09252991A
Sequence 31650, Application US/09252991A
PAPELLANT:
APPLICANT:
MARC J. Rubenfield et al.
APPLICANT:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRICK APPLICATION NUMBER: US 60/074,788
PRICK APPLICATION NUMBER: US 60/094,190
PRICK PILING DATE: 1998-02-18
PRICK PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4633, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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                        ch 25.5%; Score 58.5; DB 4; Length 396; 1 Similarity 35.7%; Pred. No. 5.2; 15; Conservative 7; Mismatches 17; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                               145 GVRPAAPADAAQRRRHHPDADHLADLGHELRQRLQRGGSRHL 186
                                                                                                                                3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GVFSAEPSPFPQTRRSMVFARHLREVGDEFR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57.5;
Pred. No. 14
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REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REALPABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 40.5
Matches 17; Conservative
                                                      Local Similarity
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                                Query Match
                                                                               Matches
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Sequence 1942. Application US/09540236

Sequence 1942. Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709-2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

EDNGTH: 373

LENGTH: 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CLOUGH, BARBARA
APPLICANT: PREISER, PETER
APPLICANT: PREISER, PETER
APPLICANT: WILSON, PARENER
TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
TITLE OF INVENTION: BEFECTIVE AS ANTI-MALARIAL COMPOUNDS
TITLE OF INVENTION: PEFECTIVE AS ANTI-MALARIAL COMPOUNDS
FILE REPERENCE: US/09/140,466
CURRENT APPLICATION NUMBER: US/09/140,466
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION UNDER: US 60/056,246
EARLIER PELING DATE: 1997-08-28
NUMBER OF SEQ ID NOS: 14
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23.8%; Score 54.5; DB 4; Length 373;
Best Local Similarity 33.3%; Pred. No. 17;
Matches 14; Conservative 7; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.8%; Score 54.5; DB 3; Length 408; Best Local Similarity 35.7%; Pred. No. 19; Matches 15; Conservative 6; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 VVSATDGPMPQTREHILLS---RQVGVPYIMVFMNKCDMVDD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 VCSAANGPWPQTREHILLA---KQVGVPYIVVFLNKADMVDD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09140466
Patent No. 6268160
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/08599480; Patent No. 5753459; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blanco, David R. APPLICANT: Miller, James N. APPLICANT: Lovett, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Cryptomonas phi
                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: M.catarrhalis
US-09-540-236-1942
                                                            US-09-540-236-1942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-140-466-4
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21338, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
TITLE OF INVENTION:
AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21338
LENGTH: 409
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APPLICANT: LYAID DOUGETEE-Stamm et al
APPLICANT: LYAID DOUGETEE-STAMM et al
APPLICANT: LYAID DOUGETEE-STAMM ANINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 032796-032
CURRENT APPLICATION NUMBER: US 6/055,778
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 4666
LENGTH: 373
                                                                                                                                                                    Gaps
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                                                                                                          Query Match
24.2%; Score 55.5; DB 4; Length 407;
Best Local Similarity 35.7%; Pred. No. 14;
Matches 15; Conservative 6; Mismatches 18; Indels
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23.8%; Score 54.5; DB 4; Length 373;
Best Local Similarity 35.7%; Pred. No. 17;
Matches 15; Conservative 6; Mismatches 18; Indels 3
                                                                                                                                                                                                                                                  115 VCSAADGPMPQTREHILLS---RQVGVPYIVVFLNKADMVDD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 VCSAADGPMPQTREHILLS---RQVGVPYIVVFLNKADMVDD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
                                                                                                                                                                                                                     3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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CRGANISM: Enterococcus faecalis
US-09-134-000C-4666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 35.7
Matches 15, Conservative
                                  ; ORGANISM: FBELLON
US-09-252-991A-21346
                                                                                                                                                                                                                                                                                                                                                                                -09-252-991A-21338
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US-09-134-000C-4666
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83 VVSAADGPMPQTREHILLSRN---VGVPYIVVFLNKMDMVDD 121

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PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 21346 LENGTH: 407

3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE

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US-09-248-796A-25524

US-09-248-796A-25524

Sequence 25524, Application US/09248796A

Sequence 25524, Application US/09248796A

Sequence 25524, Application US/09248796A

Setting No. 647137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: WOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANK

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-13

NUMBER OF SEQ ID NOS: 28208

SEQUENCE: APPLICATION NUMBER: US 60/096,409

FRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208
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                                                                         RESULT 12
US-09-187-999-15
Sequence 15, Application US/09187999A
Sequence 15, Application US/09187999A
Sequence 15, Application US/09187999A
GENERAL INFORMATION:
APPLICANT: Gindullis, Frank
TITLE OF INVENTION: Proteins that Interact with Nuclear Matrix
TITLE OF INVENTION: Proteins and Function as Transcriptional Activators
FILE REFERENCE: CL-1321
CURRENT APPLICATION NUMBER: US/09/187,999A
CURRENT PILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Microsoft Office 97
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Pred. No. 27;
3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.6%; Score 54; DB 4; Length 339; Best Local Similarity 31.8%; Pred. No. 18; Matches 14; Conservative 8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 EPSPPPOTER-----SMVFARHLREVGDE-FRSRHLNSTDDADE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 EPAPIPETSSGSLSPSPYLVNHKRRGGGEAFANRKLDGLEEAEQ 64
7 AEPDPFOPLOVARVFOR -- RVPGOECRCRH 34
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US-09-140-466-5
Sequence 5, Application US/09140466
Sequence 6, Application US/09140466
Research No. 6268160
GENERAL INPORMATION
APPLICANT: CLOUGH, BARBARA
APPLICANT: PRISER, PETER
APPLICANT: PRISON FORETER
APPLICANT: PRISON FORETER
THERE OF INVENTION AN PRE-TH DECTETA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Lycopersicon esculentum US-09-187-999-15
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Best Local Similarity 45.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
) ORGANISM: Candida
US-09-248-796A-25524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 15
LENGTH: 339
TYPE: PRT
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Dp
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Sequence 32486, Application US/09252991A
Sequence 32486, Application US/09252991A
Sequence 32486, Application US/09252991A
Sequence 32486, Application US/09252991A
SETENTIAL NEORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: APPLICATION NUMBER FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1999-07-27
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                          APPLICANT: Tempst, Paul J.
TITLE OF INVENTION: NUCLECTIDE AND AMINO ACID SEQUENCES OF A
TITLE OF INVENTION: T. Pallidum RARE OUTER MEMBRANE PROTEIN
UNDER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.6%; Score 54; DB 4; Length 267; Best Local Similarity 46.7%; Pred. No. 14; Matches 14; Conservative 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
23.6%; Score 54; DB 1; Length 242;
Best Local Similarity 38.2%; Pred. No. 12;
Matches 13; Conservative 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07419/018001 (CIP of 016001)
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INY PC compatible
COMPUTER: INY PC compatible
COMPUTER: PATENTINE PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,480
FILING DATE: 23-JAN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 PTHIPQTSRYLGSAQHLSFVGFRIRTSPSERVDD 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Learn, June M.
REGISTRATION UNDRER: 31,238
REFERENCE/DOCKET UNDRER: 07415
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 678-5070
TELEFAX: (619) 678-5099
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32486
     Cheryl I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 242 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-599-480-4
        Champion,
                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                             92037
                                                                                                                                                                                                                                                                                  COUNTRY:
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RESULT 15

US-09-252-914-32205

US-09-252-914-32205

Sequence 32205, Application US/09252991A

Petent No. 6551795

GENERAL INFORMATION:

APPLICANT NATO:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-27

LEDGTH 433

LEDGTH 433
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23.4%; Score 53.5; DB 3; Length 409;
Best Local Similarity 35.7%; Pred. No. 26;
Matches 15; Conservative 5; Mismatches 19; Indels
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TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS FILE REFERENCE: M68837B GCW PUC DP CURRAY APPLICATION NUMBER: US/09/140,466 CURRENT FILING DATE: 1998-08-26 EARLIER APPLICATION NUMBER: US 60/056,246 EARLIER FILING DATE: 1997-08-28 NUMBER OF SEQ ID NOS: 14 SEQ ID NOS: 15 SEQ ID NOS: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 VVSAADGPMPQTREHILLA---KQVGVPNMVVFLNKEDQIDD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Cyanophora paradoxa
US-09-140-466-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-32205
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Search completed: November 10, 2004, 13:44:02 Job time : 15.1986 secs

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Sequence 4781, A Sequence 52408, A Sequence 53408, A Sequence 52408, A Sequence 19, Appl Sequence 19, Appl Sequence 10, Appl Sequence 10, Appl Sequence 50956, A Sequence 50956, A Sequence 51615, A Sequence 51611, A Sequence 55414, A Sequence 65414, A Sequence 65623, A Sequence 66623, A Sequence 666623, A Seq

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5 US-10-282-122A-50564

5 US-10-282-122A-47841

5 US-10-282-122A-50484

5 US-10-282-122A-50486

5 US-10-282-122A-53962

6 US-10-067-974-14

6 US-10-067-974-14

6 US-10-067-974-14

6 US-10-077-695-19

6 US-10-771-695-19

6 US-10-771-695-10

6 US-10-771-695-10

6 US-10-771-695-10

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6 US-10-771-695-10

6 US-10-282-122A-50956

5 US-10-282-122A-62675

6 US-10-282-122A-62675

7 US-10-282-122A-62675

8 US-10-424-599-161615

7 US-10-425-114-70141

5 US-10-282-122A-65241

5 US-10-282-122A-65241

6 US-10-282-122A-65641

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US-09-815-242-12002
  RESULT 1
US-10-092-750-29
  Sequence 29, Appl
Sequence 118, Appl
Sequence 121066,
Sequence 232269,
Sequence 40545, A
Sequence 5261, A
Sequence 178354,
Sequence 178354,
Sequence 17816, A
Sequence 17610, A
Sequence 47669,
                                                                                    November 10, 2004, 16:36:12; Search time 47.2577 Seconds (without alignments) 328.807 Million cell updates/sec
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                                                                                                                                                                            44
                                                                                                                                         US-10-092-750-29
229
1 AGVFSAERSPFPQTRRSMVF.....REVGDEFRSRHLNSTDDADE
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1: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-309-290-118
US-10-417-450-8
US-10-437-963-121066
US-10-425-115-237269
US-10-425-115-240881
US-10-767-701-40881
US-10-767-701-40841
US-10-282-122A-52051
US-10-424-599-145647
US-10-282-122A-57051
US-10-282-122A-57051
US-10-282-122A-57051
US-10-282-122A-57051
US-10-282-122A-57051
US-10-282-122A-57051
US-10-282-122A-57051
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                                                                                                                                                                                                                                         1566620 segs, 353225886 residues
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                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                                                                                                                                                                                                  Scoring table:
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1555
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Maximum DB
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ALIGNMENTS

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100.0%; Score 229; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 44; Conservative 0; Mismatches 0; Indels
Sequence 29, Application US/10092750;
Sequence 29, Application US/10092751;
Publication No. US20030032157A1
GENERAL INCORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia
APPLICANT: Wright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1;
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 44
TYPE: PRI
CREATION: Homo sapiens
US-10-092-750-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGVFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
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US-10-309-290-118
US-10-309-290-118
Sequence 118, Application US/10309290
Publication No. US20040023241A1
GENERAL INFORMATION:
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1111098768482

Result

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PAPELICANT: La ROSS, Thomas J.
APPLICANT: La ROSS, Thomas J.
APPLICANT: La ROSS, Thus
APPLICANT: Zhou, Yihus
APPLICANT: Zhou, Yihus
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Britantow, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBUCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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GENERAL INFORMATION:

APPLICANT: JACKSON, Jennifer L.; BAUGHN, Mariah R.;
APPLICANT: JACKSON, Jennifer L.; BAUGHN, Mariah R.;
APPLICANT: ELLIOTT, VICKI S.; BURFORD, Neil;
APPLICANT: ELLIOTT, VICKI S.; BURFORD, Neil;
APPLICANT: CHANG, Y. TON, AZIMZAI, Yalda;
APPLICANT: CHANG, Y. TON, AZIMZAI, Yalda;
APPLICANT: CHANG, Junning: BOROWSKY, Mark L.;
APPLICANT: TONG, Junning: BOROWSKY, Mark L.;
APPLICANT: AND JACKS, Karen Anne; WARREN, Bridget,
APPLICANT: JOLLEY, Helen E.; HAFALIA, April J. A.; Hujun Z. Ring
APPLICANT: JOLLEY, Helen E.; HAFALIA, April J. A.; Hujun
APPLICANT: JOLLEY, Helen E.; HAFALIA, April J. A.; Hujun
APPLICANT: JOLLEY, Reviets B.; JOLOGES, MARCAN APPLICANTON NUMBER: US, JO, 708.9

PRIOR APPLICANTON NUMBER: US, JO, 708.9

PRIOR APPLICANTON NUMBER: US 60/285, 489

PRIOR PILING DATE: 2001-04-19

PRIOR PILING DATE: 2001-05-04

PRIOR PILING DATE: 2001-05-04

PRIOR PILING DATE: 2001-05-10

PRIOR PILING DATE: 2001-05-10

PRIOR PILING DATE: 2001-05-10

PRIOR PILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: US 60/230,369

PRIOR PILING DATE: 2001-05-11

PRIOR PILING DATE: 2001-01-05-04

PRIOR PILING DATE: 2001-05-04

PRIOR PILING DATE: 2001-05-11

PRIOR PILING DATE: 2001-01-05-04

PRIOR PILING DATE: 2001-
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100.0%; Pred. No. 2.3e-12;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 TRKSMVFARHLREVGDEFRSRHLNSTDDAD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 TRRSMVFARHLREVGDEFRSRHLNSTDDAD 43
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; OTHER INFORMATION: Incyte ID No: 7493913CD1
US-10-471-450-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 121066, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 30; Conserva
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US-10-437-963-121066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFREENCE: 21402-502A
CURRENT APPLICATION NUMBER: US/10/309,290
CURRENT FILING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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PRICR APPLICATION NUMBER: 60/336,600

PRICR FLILNG DATE: 2001-12-07

PRICR FILLING DATE: 2001-12-07

PRICR FILLING DATE: 2001-12-07

PRICR FILLING DATE: 2001-12-12

PRICR FILLING DATE: 2001-12-20

PRICR FILLING DATE: 2001-12-20

PRICR FILLING DATE: 2001-12-20

PRICR FILLING DATE: 2001-12-20

PRICR FILLING DATE: 2001-12-27

PRICR FILLING DATE: 2001-12-37

PRICR FILLING DATE: 2001-12-37

PRICR FILLING DATE: 2002-04-17

PRICR FILLING DATE: 2002-04-17

PRICR FILLING DATE: 2002-05-15

PRICR FILLING DATE: 2002-05-15
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67.7%; Score 155; DB 15; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 TRRSMVFARHLREVGDEFRSRHLNSTDDAD 265
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                                                                                                                                                                                                                                                                       Gorman, Linda
Gould-Rothberg, Bonnie E.
               Alsobrook II, John P.
Anderson, David W.
Boldog, Ferenc i.
Burgess, Catherine E.
Chillakuru, Rajeev A.
Edinger, Shlomit R.
Gerlach, Valerie L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rastelli, Luca
Rieger, Daniel K.
Shenoy, Suresh G.
Smithson, Glenda
Starling, Gary
Taupier, Raymond J.
Voss, Edward Z.
Zhong, Haihong
                                                                                                                                                                                                                                                                                                                                                                                 Jeffers, Michael E.
Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malyankar, Uriel M.
Miller, Charles E.
Murphey, Ryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patturajan, Meera
Peyman, John A.
                                                                                                                                                                                                                                                                                                                                                                 Suo, Xiaojia
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GRGANISM: Homo sapiens
US-10-309-290-118
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US-10-471-450-8; Sequence 8, Application US/10471450; Publication No. US20040152877A1

Gaps

4

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Query Match 26.6%; Score 61; DB 17; Length 414; Best Local Similarity 50.0%; Pred. No. 12; Matches 14; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.6%; Score 61; DB 16; Best Local Similarity 50.0%; Pred. No. 13; Matches 14; Conservative 2; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.6%; Score 61; DB 16; Best Local Similarity 50.0%; Pred. No. 13; Matches 14; Conservative 2; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 EPSPFAYISGYKNRFQNFIKHIREMGDE 54
                                                                                                                                   7 EPSPFP----QTRRSMVFARHLREVGDE 30
                                                                                                                                                                                33 EPSPFAYISGYKNRFONFIKHLREMGDE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-437-963-178354
; Sequence 178354, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Oryza sativa
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US-10-425-115-240881
i Sequence 240881, Application US/10425115
j Publication No. US20040214272A1
j GENERAL INFORMATION:
j APPLICANT: La Rosa, Thomas J.
j APPLICANT: Canou, Yihua
j APPLICANT: Canou, Yihua
j APPLICANT: Canou, Yihua
j TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
j TITLE OF INVENTION: Plants
j CURRENT APPLICATION NUMBER: US/10/425,115
j CURRENT APPLICATION NUMBER: 2003-04-28
j NUMBER OF SEQ ID NOS: 369326
j SEQ ID NO 240881
j LENGTH: 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-425-115-237269

US-10-425-115-237269

Sequence 237269, Application US/10425115

Sequence 237269, Application US/10425115

Sequence 237269, Application US/20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants

FILE OF INVENTION: Plants

FILE SEFERENCE: 38-21(53222)

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 237269

LENTH: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                                                                                                                                                                 Query Match 27.5%; Score 63; DB 16; Length 415; Best Local Similarity 46.9%; Pred. No. 6.5; Matches 15; Conservative 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.6%; Score 61; DB 17; Length 77; Best Local Similarity 50.0%; Pred. No. 1.7; Matches 14; Conservative 2; Mismatches 8; Indels
                                                                                                                                                    FEATURE:

CTHER INFORMATION: Clone ID: PAT_MRT4530_24127C.1.pep

US-10-437-963-121066
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US-10-425-115-240881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: MRT4577_147975C.1.pep
US-10-425-115-237269
                                                                                                                                                                                                                                                                                                                                                                         3 VFSAEPSPFP----QTRRSMVFARHLREVGDE 30
                                                                                                                                                                                                                                                                                                                                                                                                        30 VLFVEPSPFAXISGYKNRFQNFIKHLREMGDE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 EPSPFP----OTRRSMVFARHLREVGDE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 EPSPFAYISGYKNRFQNFIKHLREMGDE 34
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 121066
LENGTH: 415
                                                                                                          TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
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APPLICANT: La Rovalic, David K.
APPLICANT: La Kovalic, David K.
APPLICANT: Excalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwa
APPLICANT: Cao, Yongwa
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Brad
APPLICANT: Buckharov, Brad
APPLICANT: Buckharov, Brad
APPLICANT: Buckharov, Brad
APPLICANT: Brancharov, Brad
APPLICANT: Brancharov, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 178354
US-10-767-701-40545

US-10-767-701-40545

Sequence 40545, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:
APPLICANT: ADAU, Yihua

APPLICANT: APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: NUMBER: US/10/767,701

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 40545

LENGTH: 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C82521_1.pep
US-10-767-701-40545
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US-10-437-963-178354
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Gaps

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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF EEQ ID NOS: 285684 SEQ ID NO 145647 LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.8%; Score 59; DB 15; Length 266; Best Local Similarity 35.6%; Pred. No. 13; Matches 16; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 PFPQ-----TRRSMVFAR--HIREVGDEFRSRHINSTDDADE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 PFPNSNASSPVFTVRASVFAQWPHLRYFSSDKKDDHSDEDDDGDE 75
                                                                                                                                                                                                                                                                        FEATURE:

NAME/KEY: Unsure

LOCATION: (1). (266)

OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_102538C.1.pep
US-10-424-599-145647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57410, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Ohlsen, Kari
Zyskind, Judith
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-282-122A-57410
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: BLITRA,134A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PRILING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-16
PRIOR PRILING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PRILING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR D
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Pred. No. 13;
4; Mismatches 19;
               ||||||
EPSPFAYISGYKNRFQNFIKHLREMGDE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 145647, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                     Sequence 52051, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium acetobutylicum
                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
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26.4%;
Best Local Similarity 38.1%;
Matches 16; Conservative
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APPLICANT: Foreyth, R. TILLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/202,122A
CURRENT FILING DATE: 2000-03-02
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,35
PRIOR PELING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-29
PRIOR PLING DATE: 2000-12-29
PRIOR PLING DATE: 2000-12-29
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-04
PRIOR PLI
Sequence 52391, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                               Zyskind, Judith
Wall, Daniel
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APPLICANT:
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AU, M.,
FILE REFERENCE: ELITRA 034A
CURRENT APPLICATION NUMBER: 02/10/282,122A
CURRENT FILING DATE: 2000-3-02-02
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/207,127
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-00-6
PRIOR PLING DATE: 2000-00-6
PRIOR PLING DATE: 2000-00-6
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-26
PRIOR PLING DATE: 2000-12-6
PRIOR PLING DATE: 2000-12-6
PRIOR PLING DATE: 2001-12-7
PRIOR PLING DATE: 2001-12-6
PRIOR PLING DATE: 2001-12-6
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-03-16
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                                                                                                                                            DB 15; Length 282;
                                                                                                                                       Score 58.5; DB 15; Length Pred. No. 17; 7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Indels
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                                                                                                                                                                                                                                                                                                               3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
                                                                                                                                                                                                                                                                                                                                                                          17 VVSATDGPMPQTREHILLS---RQVGVKYLIVFLNKVDLVDD 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
25.1%; Score 57.5; D
Best Local Similarity 38.1%; Pred. No. 16;
Matches 16; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 47669, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; ORGANISM: Burkholderia cepacia
US-10-282-122A-47669
             ; ORGANISM: Enterococcus faecium US-10-282-122A-57410
                                                                                                                                   Query Match
Best Local Similarity 35.7%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto, Robert
Forsyth, R.
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Carr, Grant
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                                                                   Query Match
25.1%; Score 57.5; DB 15; Length 235;
Best Local Similarity 35.7%; Pred. No. 18;
Matches 15; Conservative 5; Mismatches 19; Indels 3;
                                                                                                                                                                                 3 VFSAEPSPFPOTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
                                                                                                                                                                                                                                                                                           Sequence 50564, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
APPLICANT: Wang, Liangsu APPLICANT: Mandio, Carlos APPLICANT: Malone, Cheryl APPLICANT: Hasilbeck, Robert
TYPE: PRT ORGANISM: Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trawick, John
Carr, Grant
Yamamoto, Robe:
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
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RESULT 13 US-10-282-122A-52391

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CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PPLICANT: Xu, H. (The control of Essential Genes in Microorganisms)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57.5; DB 15; Length
Pred. No. 32;
5; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 VCSAADGPMPQTREHILLA---RQVGVPYIIVFLNKCDMVDD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
                                            TILE REFERENCE: ELITRA, 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/20

PRIOR PILING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/22,625

PRIOR APPLICATION NUMBER: 60/25,625

PRIOR APPLICATION NUMBER: 60/25,625

PRIOR APPLICATION NUMBER: 60/25,635

PRIOR APPLICATION NUMBER: 60/25,635

PRIOR APPLICATION NUMBER: 60/25,931

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/25,931

PRIOR APPLICATION NUMBER: 60/26,308

PRIOR APPLICATION NUMBER: 60/26,308

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 47841, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ION NUMBER: 60/230,335
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APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-10-282-122A-50564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 38.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-282-122A-47841
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                    Copyright
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- protein search, using sw model OM protein

November 10, 2004, 12:29:32; Search time 9.80311 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

44

US-10-092-750-29 229 1 AGVFSAEPSPFPQTRRSMVF.....REVGDEFRSRHLNSTDDADE Perfect score: Sequence: Title:

Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	hypothetical prote	c	n Fa	hypothetical prote	cal	ion	ation	ion		ion	tion	tion	elong	pox	fact	io io		щ	trans	11	ion	tion e	n trans	at	ion	tion el	•	ion fac	transcription fact
2417777700	ID	147	ø	H97285	735	T45962	EFYMTS	855281	A82532	G87143	823909	800229	S17146	829293	A87330	AC2818	C97596	AB2816	D97594	AE3346	A44795	T44381	140216	4	1016	8123	812	E86857	8311	5374
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•	Length	ന	(T)	397	0	7	(D)	a)	Q)	O)	σn.	0	0	0	r	σ	σ	σ	σ	σ	σ	o,	g,	0	σ	O)	394	σı	σ	0
% Query	Match	67.7	26.4	26.4			25.5			25.1		25.1	25.1	25.1			24.7			24.7	24.7						24.2			
	Score	Ω	ö		σ,	59	8	8	58.5	۲.	۲.	۲.	7	7	7.	9	9	ė.	ů.	ė.	ů.	ů.	ů.	9	ъ.	'n.	ď.	ď.	'n	'n
Result	No.	н	7	e	4	2	9	7	œ	თ	10	11		13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	.28	58

26.4%; Score 60.5; DB 2; Length 396; 38.1%; Pred. No. 3.6;

Query Match Best Local Similarity

probable 2,3-dihyd conserved hypothet	translation elonga	-	translation elonga	translation elonga	translation elonga	translation elonga	fzr related protei	probable outer mem	hypothetical prote	translation elonga		translation elonga	translation elonga
B40626 A69793	A81392	C60663	\$73208	S68466	S62768	S62767	T49342	H71297	T37690	C71672	AD1406	AD1782	A87403
01 01	01 0	N (V	2	N	~	N	7	N	~	7	~	7	N
250 827	399	405	409	452	452	452	849	242	844	394	395	395	396
24.0	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.6	23.6	23.4	23.4	23.4	23.4
55 24.0 55 24.0		54.5 23.8						4.	54 23.6			53.5 23.4	

# ALIGNMENTS'

RESULT

T14795
hypothetical protein DKFzp434E171.1 - human (fragment)
C;Species: Homo sapiens (man) C;Date: 20-Sep.1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: 114'). R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A)Accession: Induct: 210103
A;Status: preliminary A;Molecule type: manna, * notice the manna
A)KeBiddes: 1-383 <poo. A)Cooss-references: EMBL:AL110285 A.Twravimental course. Adult testis. Clone DKP2n414R171</poo. 
Query Match Best Local Similarity 100.0%; Pred. No. 1.2e-12; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 TRRSMVFARHLREVGDEFRSRHINSTDDAD 43
Db 239 TRRSMVFARHIREVGDEFRSRHINSTDDAD 268
RESULT 2
boves. Los partion elongation factor EF-Tu - Pseudomonas cepacia Cosperias: Pseudomonas cepacia
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jul-2004
R; Ludwig, W.; Neizenegger, M.; Betzl, D.; Leidel, E.; Lenz, T.; Ludvigsen, A.; Moellenhof
AICH: MICLOMICE, 133, 241 241, 133, A/TILL COMPLET uncleotist sequences of seven eubacterial genes coding for the elongat: 1.Pafarence number: A60663: MITD:90240875; PMID:2110445
A; Accession: December : Accession: December
A; status: not compared with conceptual translation A; Molecule type: DNA
A;Residues: 1-396 <lud> A;Cross-references: UNIPROT:P33167</lud>
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog C;Seywords: GTP Station; nucleotide binding; P-loop; protein biosynthesis F:13-13-13-17-15-17-15-17-17-17-17-17-17-17-17-17-17-17-17-17-
F;19-26/Region: nuclectide-binding motif A (P-loop) F;136-139/Region: GTP-binding NKXD motif
F;174-176/Region: GTP-binding SAK/L motif F;25,26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #stat

d

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C.Accession: S55281; S52237,
A.S. Faremaud, L.; Fremaux, C.; Laalami, S.; Cenatiempo, Y.
Nucleic Acids Res. 23, 1737-1743, 1995
A,Title: Genetic and molecular analysis of the tRNA-tufB operon of the myxobacterium Stig
A,Reference number: S55281; MUID:95303606; PMID:7784178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Generic code: SGC3
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
C; Superfamily: translation elongation factor Tu; translation biosynthesis
C; Syporation: translation elongation factor Tu homology «ETU»
F; 13-139 / Domain: translation elongation factor Tu homology «ETU»
F; 19-26/Region: nucleotide-binding motif A (P-loop)
F; 19-136/139/Region: GTP-binding NKXD motif
F; 174-176/Region: GTP-binding SAK/L motif
F; 25, 26, 62, 136, 137, 139, 174/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #stat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-394 < INA>
A; Cross_references: UNIPROT: P18906; EMBL: X16462; NID: g44292; PIDN: CAA34482.1; PID: g44293
                                                                                                                                                            A; Cross-references: UNIPROT:Q9LFB4; EMBL:AL137189
A; Experimental source: cultivar Columbia; BAC clone F7J8
C; Genetics:
A; Map position: 5
A; Inap position: 5
A; Inap costion: 5
A; Inap costion: 5
A; Note: F7J8.200
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A;Molecule type: DNA
A;Residues: 1-396 <BRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation elongation factor EF-Tu - Mycoplasma gallisepticum C; Species: Mycoplasma gallisepticum C; Species: Mycoplasma gallisepticum C; Species: Mycoplasma gallisepticum C; State: 31-Dec-1991 #Sequence_revision 31-Dec-1991 #text_change 09-Jul-2004 C; Accession: S14910; S06704 R; Inamine, J.M.; Loechel, S.; Hu, P.C. Nucleic Acids Res. 17, 10126, 1989 A; Title: Nucleotide sequence of the tuf gene from Mycoplasma gallisepticum. A; Reference number: S14910; MUID:90098800; PMID:2602129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation elongation factor BF-Tu - Stigmatella aurantiaca
C;Species: Stigmatella aurantiaca
C;Date: 23-Aug.1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: S55281; S52237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 6.5;
4; Mismatches 18; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                            Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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submitted to the Protein Sequence Database, January 2000
A,Reference number: Z23018
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.8%; Score 59; DB 2; Best Local Similarity 50.0%; Pred. No. 6.8; Matches 14; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||
111 EPSPFAYVSGYKNRFQNFIRYLREMGDE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 EPSPFPQT----RRSMVFARHLREVGDE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 40.5%;
Matches 17; Conservative 4
                                                                                                                           A; Molecule type: DNA
A; Residues: 1-470 <BEV>
                                                        A, Accession: T45962
A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
ÈFYMTS
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                                                                                                                                                                                                           RESULT 3
H97285
elongation Factor Tu (Ef-Tu) [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97285
R;Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A;Eacteriol. 183, 4833-4838, 2001
A;Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
145962
hypothetical protein F7J8.200 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45962
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CAC3136
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:062499; EMBL:299283; PIDN:CAB16537.1; GSPDB:GN00023; CESP:Y7; Experimental source: clone Y70C5C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .Cross-references: UNIPROT:097EH5; GB:AE001437; PIDN:AAK81075.1; PID:g15026203; GSPDB:
.Experimental source: Clostridium acetobutylicum ATCC824
   ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y70C5C.1 - Caenorhabditis elegans
C)Species: Caenorhabditis elegans
C)Species: Caenorhabditis elegans
C)Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C)Accession: T27351
R)Steward, C.
A;Reference number: Z20351
A;Reference number: Z20351
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Indels
                                                                                                   VSAADGPMPQTREHILLA---SRVGVEYIVVFLNKADGVDD 143
                                                           3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60.5; DB
Pred. No. 3.6;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59.5; DE
Pred. No. 3.6;
5; Mismatches
   Mismatches
   ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 39.5%;
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 38.1%;
Matches 16; Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-397 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: CESP:Y70C5C.1
A,Map position: 5
A,Introns: 113/1; 225/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -301 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
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Matches
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Eur. J. Biochem. 170, 93-98, 1987
A;Title: Molecular cloning and sequence determination of the tuf gene coding for the elor
A;Reference number: S00229; MUID:88082865; PMID:2826164
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87143
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R;Cole, S.T.; Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, Title: Massive gene decay in the leprosy bacillus.
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: G87143
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-396 cSTO>
A;Accession: Manney
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P30768; GB:AL450380; NID:gl3093557; PIDN:CAC30831.1; GSPDB:Gh C;Genetics:
A;Gene: tuf
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
Residues: 1-397 <WON>
A;Cross-references: UNIPROT:P29543; EMBL:X67058; NID:g47485; PIDN:CAA47443.1; PID:g581733
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lys, Asp, Ser) #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation elongation factor EF-Tu.A version 1 [validated] - Thermus aquaticus N;Contains: GTPase (EC 3.6.1.-) (Species: Thermus aquaticus C;Species: Thermus aquaticus C;Date: 14-Aug-1998 #text_change 09-Jul-2004 C;Accession: S00229; A27277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Astart codon: GTG
C; Superfamily: translation elongation factor Tu; translation elongation factor C;
C; Superfamily: translation elongation factor Tu homology <ETU>
C; Start Codon: translation elongation factor Tu homology <ETU>
F; 19-2-65 Region: mucleotide-binding motif A (P-loop)
F; 138-141 Region: GTP-binding NXXD motif
F; 176-178 Region: GTP-binding SAX/L motif
F; 25, 26, 64, 138, 139, 141, 176/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation elongation factor EF-Tu.2 - Streptomyces ramocissimus
C;Species: Streptomyces ramocissimus
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.1%; Score 57.5; DB 2; Length 3 Best Local Similarity 35.7%; Pred. No. 8.9; Matches 17; Indels Matches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Kushiro, A.; Shimizu, M.; Tomita, K.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S00229
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ASS532

ASS62

C,5pecies: Nylelia fastidiosa

R, anonymous, The Xylelia fastidiosa

A,5pecies: Nylelia fastidiosa

A,5pecies: Nylelia

A,
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                                                                                                                                                                                             Lys, Asp, Ser)
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llarity 38.1%; Pred. No. 6.5;
Conservative 5; Mismatches 18; Indels
                                                                                                                                                                                                                                                          Score 58.5; DB 2; Length 396;
Pred. No. 6.5;
5; Mismatches 18; Indels
                     C,Keywords: GTP binding; nucleotide binding; P-loop F;13-139/Domain: translation elongation factor Tu homology <ETU>F;19-26/Region: nucleotide-binding motif A (P-loop) F;136-139/Region: GTP-binding NKXD motif F;174-176/Region: GTP-binding SAK/L motif F;25,26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Thr, Thr, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 VVSAADGPMPQTREHILLA---RQVGVPYIVVFLNKVDMLDD 143
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                                                                                                                                                                                                                                                                                                                                                                                                            3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
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elongation factor EF-Tu [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
                                                                                                                                                                                                                                                              25.5%;
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 38.1
Matches 16; Conservative
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hes 16; Conserv
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ð 셤

Tu homolog

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AAccession: $22233
A,Molecule type: DNA
A,Residues: 1.406 «VOS.
A,Reperimental source: strain EPOOR276
R, Poblekhina, G, Thirup, S.; Rieldgaard, M.; Nissen, P.; Lippmann, C.; Nyborg, J.
A,Reference number: A67699; PDB:1TUI
A,Rote: strain yt.
B,Note: strain yt.
A,Rote: strain yt.
B,Note: strain yt.
A,Rote: strain yt.
B,Note: strain yt.
B,Rissen, P.; Keledgaard, M.; Thirup, S.; Polekhina, G.; Reshetnikova, L.; Clark, B.F.C.;
Science 270, 1464-1472, 1995
A,Title: Crystal structure of the ternary complex of Phe-tRNA(Phe), EF-Tu, and a GTP anal
A,Reference number: A57609; MUID:96095207; PMID:7491491
A,Reference number: A57609; MID:93182488; PMID:371755
A,Title: Crystal structure of active elongation factor Tu reveals major domain rearrangen
A,Reference number: A5889; MID:9317755
A,Reference number: A5889; MID:9317755
                                                                                                                                                                                                                                                                                                                  A, Contents: annotation; X-ray crystallography, 2.7 angstroms
R;Berchtold, H.; Reshetnikova, L.; Reiser, C.O.; Schirmer, N.K.; Sprinzl, M.; Hilgenfeld,
Mautre 365, 126, 1993
A;Title: Crystal structure of active elongation factor Tu reveals major domain rearrangen
A;Reference number: A58849; MUID:93382498; PMID:8371755
A;A;Contents: annotation, X-ray crystallography, 1.7 angstroms
C;Comment: Translation elongation factor Tu is the archetypal guanine nucleotide binding
A:ribosome complex. Recycling of the inacvtive GDP complex is catalysed by translation el
                                                                                                                             RiNissen, P.; Kjeldgaard, M.; Thirup, S.; Polekhina, G.; Reshetnikova, L.; Clark, B.F.C.; Science 270, 1464-1472, 1995
A;Title: Crystal structure of the ternary complex of Phe-tRNA(Phe), EF-Tu, and a GTP anal A;Reference number: A57609; MUID:96095207; PMID:7491491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C'Superfamily: translation elongation factor Tu; translation elongation factor Tu homology. Superfamily: binding; hydrolase; nucleotide binding; P-loop; protein biosynthesis F;13-140/Domain: translation elongation factor Tu homology «ETU»
F;19-26/Region: nucleotide-binding motif A (P-loop)
F;137-140/Negion: GTP-binding Nat MCD motif F;173-140/Negion: GTP-binding Nat McD motif F;15-177/Region: GTP-binding sak/L motif F;25,26,63,137,138,140,175/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #stat
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C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: S;29293
FyVoss, R.H.; Hartmann, R.K.; Lippmann, C.; Alexander, C.; Jahn, O.; Erdmann, V.A.
Bur. J. Blochem. 207, 833-846, 1992
A;Title: Sequence of the tufA gene encoding elongation factor EF-Tu from Thermus aquation
A;Reference number: S;29293; MUID:92362620; PMID:1499561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Contents: annotation, X-ray crystallography, 1.7 angstroms
C;Comment: Translation elongation factor Tu is the archetypal guanine nucleotide binding
A:ribosome complex. Recycling of the inacvtive GDP complex is catalysed by translation el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
K*Ewwords: GTP binding; hydrolase; nucleotide binding; P-loop; protein biosynthesis
F;13-140/Domain: translation elongation factor Tu homology <BTU>
F;19-26/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 406;
                                             A, Contents: annotation; X-ray crystallography, 2.7 angstroms A, Note: strain yt-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 VVSAADGPMPQTREHILLA---RQVGVPYIVVFMNKVDMVDD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation elongation factor EF-Tu.A version 2 [validated] N.Contains: GTPase (EC 3.6.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.1%; Score 57.5; DB 1;
35.7%; Pred. No. 9.1;
live 6; Mismatches 18;
A; Reference number: A67698; PDB:1TUI
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es 15; Conservative
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Matches
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                         A; Residues: 1-406 «KUS»

A; Residues: 1-406 «KUS»

A; Essidues: 1-406 «KUS»

A; Essidues: 1-406 «KUS»

A; Essidues: 1-406 «KUS»

A; Essidues: 1-406 «KUS»

A; Ester, mental source: strain HB8

A; Note: the source is designated as Thermus thermophilus HB8

B; Seidler, L.; Peter, M; Meissner, F.; Sprinzl, M.

Nucleic Acids Res. 15, 9263-9277, 1987

A; Title: Sequence and identification of the nucleotide binding site for the elongation for A; Reference number: A27277; MUD: 88067755; PMID: 3317278

A; Molecule type: DA;

A; Residues: 1-379, G', 381-406 «SEI»

A; Residues: 1-379, G', 381-406 «SEI»

A; Note: the source is designated as Thermus thermophilus HB8

A; Note: the source is designated as Thermus thermophilus HB8

A; Note: the source is designated by amino acid analysis

A; Note: the source is designated by amino acid analysis

B; Polekhina, G; Thirup, S; Kjeldgaard, M.; Nissen, P; Lippmann, C; Nyborg, J.

Submitted to the Brookhaven Protein Data Bank, May 1996

A; Contents: annotation; X-ray crystallography, 2.7 angstroms
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$17146

N; Contains: Great (EC 3.6.1.-)
C; Species: Thermus aquaticus
N; Contains: Great (EC 3.6.1.-)
C; Species: Thermus aquaticus
C; Date: 14-Aug.1998 #sequence_revision 14-Aug.1998 #text_change 09-Jul-2004
C; Accession: $17146
R; Satoch, M; Tanaka, T.; Kushiro, A.; Hakoshima, T.; Tomita, K.
FEBS Lett. 288, 98-100, 1991
A; Title: Molecular cloning, nucleotide sequence and expression of the tufB gene encoding
A; Accession: $17146
A; Molecule type: DNA
A; Accession: $17146
A; Molecule type: DNA
A; Cross-references: UNIPROT: P60338; UNIPROT: P60339; EMBL: X61957; NID: 9312959; PIDN: CAA43
A; Cross-references: UNIPROT: Standard as Thermus thermophilus
A; Experimental source: strain HBB
A; Note: the source is designated as Thermus thermophilus
A; Experimental source: Strain HBB
A; Note: the source is designated as Thermus thermophilus
B; Polekhina, G; Thirup, S.; Kjeldgaard, M; Nissen, P.; Lippmann, C.; Nyborg, J.
Submitted to the Brookhaven Protein Data Bank, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Nissen, P.; Kjaldgaard, M.; Thirup, S.; Polekhina, G.; Reshetnikova, L.; Clark, B.F.C. Science 270, 1464-1472, 1995
Science 270, 1464-1472, 1995
A.Title: Crystal structure of the tronspread of Phe-tRNA(Phe), EF-Tu, and a GTP and A.Reference number: A57609; MUID:9605207; WID:7491491
A.Contents: annotation; X-ray crystallography, 2.7 angstroms
A.Fleatchhold, H.; Reshetnikova, L.; Reiser, C.O.; Schirmer, N.K.; Sprinzl, M.; Hilgenfeld Nature 365, 126, 1993
A.Title: Crystal structure of active elongation factor Tu reveals major domain rearrange A.Title: Crystal structure of active elongation factor Tu reveals major domain rearrange A.Fleference number: AS8849; MUID:93382498; PMID:8371755
A.Fleference number: A58849; MUID:93182498; PMID:8371755
A.Gontents: annotation; X-ray crystallography, 1.7 angstroms
C.Genetics: A.F.Tuf
A.Poscription: transports aminoacylated transfer RNAs to the messenger RNA:ribosome comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: binds GTP/GDP; catalyses the hydrolysis of GTP A; Description: binds GTP/GDP; catalyses the hydrolysis of GTP A; Note: the complex with GTP is active; the complex with GDP is inactive; recycling of the C; Superfamily: translation elongation factor Tu; translation elongation factor Tu; homology c; STB-140/Domain: translation alongation factor Tu homology c; P:13-140/Domain: translation alongation factor Tu homology c; P:19-26/Region: nucleotide-binding motif A (P-loop)
F:137-140/Region: GTP-binding SAK/L motif
F:151-177/Region: GTP-binding SAK/L motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thr, Thr, Asn, Lys, Asp, Ser) #sts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57.5; DB Pred. No. 9.1; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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nes 15; Conservative
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R;Nissen, P.; Kjeld
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106

ઠે g

Best Loca Matches

100 VCSAADGPMPQTREHILLA---RQVGVPAIVVFLNKVDQVDD 138

g

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Search completed: November 10, 2004, 13:40:37
                                                                                                                          Job time : 9.80311 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 Heequence_revision 20-Apr-2001 Htext_change 09-Jul-2004
C;Accession: A87330 Heequence_revision 20-Apr-2001 Htext_change 09-Jul-2004
C;Accession: A87330 Heequence_revision 20-Apr-2001 Htext_change 09-Jul-2004
C;Accession: A87330 Heequence_revision 20-Apr-2001 Htext_change 09-Jul-2004
B;Nierman, W.C; Peldblyum, T.V; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
F;137-140/Region: GTP-binding NKXD motif
F;175-177/Region: GTP-binding SAK/L motif
F;25,26,63,137,138,140,175/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
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A,Residues: 1-391 «KUR»
A,Cross-references: UNIPROT:Q8UE16; GB:AE008688; PIDN:AAL42961.1; PID:g17740420; GSPDB:G
A,Experimental source: strain CS8 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9AAE9; GB:AE005673; NID:g13421867; PIDN:AAK22637.1; GSPDB:(
C;Genetics:
A;Gene: CC0652
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Accession: AC2818
Status: preliminary
                                                                                                                                                                                         Gaps
                                                                                                                          Query Match
25.1%; Score 57.5; DB 1; Length 406;
Best Local Similarity 35.7%; Pred. No. 9.1;
Matches 15; Conservative 6; Mismatches 18; Indels 3
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                                                                                                                                                                                                                                                                                            106 VVSAADGPMPQTREHILLA---RQVGVPYIVVFMNKVDMVDD 144
                                                                                                                                                                                                                                                 3 VFSAEPSPFPQTRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
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Best Local Similarity 38.1%;
Matches 16; Conservative
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Best Local Similarity 44.7
Matches 17; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 12:27:34; Search time 53.7271 Seconds (without alignments) 471.205 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-092-750-29 229 1 AGVFSAEPSPFPQTRRSMVF.....REVGDEFRSRHLNSTDDADE 44

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	homo	homo	pan tro	рошо	Aah64623 homo sapi	Q6pjv1 homo sapien	Aah11044 homo sapi	E	Q7yrr5 bos taurus		gallu	fugn		Q7yzs7 ciona intes							Q8kmr4 lactobacill			Q6ev55 caenorhabdi	Ę,	Aar25433 lactobaci	ď	~	Q8kh86 lactobacill	Q8khj6 lactobacill	Q8khj7 lactobacill
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Q8khj8 lactobacill Q8khm4 lactobacill Q8kml3 lactobacill		Q8kmn5 lactobacill Q8kmn6 lactobacill Q8kmn7 lactobacill		Q9ezxy enterococou Q88ve0 lactobacill Q84qbl oryza sativ
ОВКНЈВ ОВКНМ4 ОВКМ1.3	QBKML5 QBKML5 QBKMM0	QBKMN5 QBKMN6 QBKMN7	OBKMR5 OBKMR6	O9EZX9 EFTU LACPL Q84QB1
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ALIGNMENTS

RESULT 1

PET; 424 AA. OFUZAL HUMAN STANDARD; OFDGS; OSUFY3; OFUZAL HUMAN STANDARD; Created C. OFUZAL HUMAN STANDARD; Created C. OFUZAL STANDARD; Created C. OFUZAL STANDARD; Created C. OFUZAL STANDARD; Created C. OFUZAL STANDARD; NAMMADIA; SHAZAAA, CRATALARA; Vertebrata; Euteleostomi; NAMMADIA; SULFARAA A., TANDARD; (I) TISSUEDER FROM N.A. (ISOFORM A). TISSUEDER FROM N.A. (ISOFORM B). THE COMPLE OF COMPLETED TO THE COMPLETED TO																III.	d)															×	, , D			:	н.,	:				an	
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		MAN	Q8WW	2000	2003	iose pi	le 0-fı	FUT2;	piens ta: Me	a; Eut	XID=96	200	Brain	=99246	3T 2	tion o	plete	ge pro		E FROM	O., Re	80, a	into	ed (Di	E FROM	Testi:	A.,	ed (At	, ea	=2028	Σ.	.S-	A., Me	1d K.,	lal A.,	na S.,	×	J., Be	er S.	H . , H 1	405:31	FINCTION:	
	TUMAN	FU2_HL	39Y2G5;	0 - MAY-	- 427 - 82 - 7017 - 3(DP-fuc	(Peptic	Jame=PC	John Sa	[amma]	CBI_Ta	[1] POTTENI	I SSUE	EDLINE	agase Hystir	Predic	the con	Or Lai	12]	SEQUENC	fenzel	C2lorf	nsignt	Submitt [2]	SECUENC	TISSUE-	Poustka	Submitt	L4J ROTTENC	TEDLINE	iattori	erk H.	olley	Reichwe	Sosenti	inoshi Tinoshi	scharfe	Ramser	Vehrmey	ehraci	Jature	F177 - 1-	
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QGEV56
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                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENE OUT statement the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@labseib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                             N-linked (GlcNac. .) (Potential).
N-linked (GlcNac. .) (Potential).
N-linked (GlcNac. .) (Potential).
CLPTSLSAESGSGGFQRFFCPKYSVSEQMVACVHSGHFHTV
-!- CATALYTIC ACTIVITY: Transfers an alpha-L-fucosyl residue from GDP-beta-L-fucose to the serine hydroxy group of a protein acceptor.
-!- PATHWAY: Glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martinez-Dunker I., Mollicone R., Candelier J.J., Breton C., Oriol R., "A new superfamily of protein-O-fucosyltransferases, alpha2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                       GDP-fucose protein O-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLIV -> ETPGEGCPHOPIORVCGGGLDLRDVYCASG
(in isoform C)
/FTIG=VSP 003832
RC -> SS (in isoform B).
/FTIG=VSP 003833.
Missing (in isoform B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                 IsoId=Q9Y2G5-3; Sequence=VSP_003832;
SIMILARITY: Belongs to the glycosyltransferase family 68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.7%; Score 155; DB 1; Length 424; 100.0%; Pred. No. 2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Protein-O-fucosyltransferase (C21orf80 protein, isoform C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                       Alternative splicing, Fucose metabolism, Glycoprotein, Glycosyltransferase, Signal, Transferase.
                                                                                                            IsoId=Q9Y2G5-2; Sequence=VSP_003833, VSP_003834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60BA687F0DFB8875 CRC64;
                                                                 Event=Alternative splicing; Named isoforms=3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    429 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 TRRSMVFARHLREVGDEFRSRHLNSTDDAD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 TRRSMVFARHLREVGDEFRSRHLNSTDDAD 43
                                                                                        Isold=Q9Y2G5-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                               Potential
                                                                                                                                                                                                                                                         EMBL; AB023175; BAA76802.1; ALT_INIT.
EMBL; AJ3020080; CAC24557.1; -.
EMBL; AJ302079; CAC24556.1; -.
EMBL; AY066015; AAL47681.1; -.
                                                                                                                                                                                                                                                                                                      EMBL, AL110285; CABS3715.1; ALT_INIT.
EMBL, AL163301; CAB90496.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 AA; 48895 MW;
                                                                                                                                                                                                                                                                                                                                                 Glycosyltransferase; Signal; SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=FUT13; Synonyms=POFUT2;
                                                                                                                                                                                                                                                                                                                             Genew; HGNC:14683; POFUT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381
                                                                                                                                                                                                                                                                                                                                                                                              2009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                             Name=A;
                                                                                                                        Name=C
                                                                                                   Name=B
                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q7Z4N0;
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**X ** **EDLINE=22388257; PubMed=12477932; Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Felngold E.A., Grouse L.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Dittchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Brotheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Richards S., Worley K.C., Hale S., Garcia A.M., Cay L.J., Hulyk S.W., Pethy J., Helton B.K., Kureman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Marra M.J., Schmutz J., Myers R.M., Butterfield Y.S., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., A Jones S.J., Marra M.A., Smailus D.E., Schnerch A., Schein J.E., Charter M., Meden A., Marra M.A., Touchman J.M., Green E.D., Dickson M.C., Anders S.J., Marra M.A., Smailus D.E., Schnerch A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .; IEA
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fucosyltransferases, and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs.";
Glycobiology 13:1c-5c(2003).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Strausberg R.;
Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ575591; CAE01472.1; -.
EMBL; BC064623; AAH64623.1; -.
GQ; GO:0016757; F:transferase activity, transferring glycosyl. ..
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Martinez-Duncker I., Oriol R., Mollicone R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosyltransferase; Transferase.
SEQUENCE 429 AA; 49975 MW; 36A4213D905AFFD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TremBirel. 28, Created)
(TremBirel. 28, Last sequence update)
(TremBirel. 28, Last annotation update)
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PubMed=12966037
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Whiting M., Madan A., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                    FROM N.A.
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                                                                                                                                                                                                                                                            TISSUE=Brain;
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                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pad-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Menzel O., Reymond A., Antonarakis S.E., Guipponi M.;
Disruption and overexpression of the Caenorhabditis elegans pad-2
"Disruption and overexpression of the Caenorhabditis elegans pad-2
gene revealed possible roles (r C21orf80, its human ortholog, in pathogenesis of Down syndrome.";
pathogenesis of Down syndrome.";
Submitted (ANG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY066015, AAL4/881.2;
SEQUENCE 429 AA, 49975 MW; 36A4213D905AFFDI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
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Catarrhini, Hominidae, Homo.
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                                                                                                  Length 429;
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         EMBL; AJ781756; CAH03731.1; -.
Glycosyltransferase; Transferase.
SEQUENCE 429 AA; 49846 MW; 77A3635BD4698983 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
C210rf80 protein, isoform C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.7%; Score 155; DB 2;
100.0%; Pred. No. 2e-11;
ive 0; Mismatches 0
                                                                                                Score 155; DB 2;
Pred. No. 2e-11;
                                                                                                                                                                                                                                                                                                                                                     429 AA.
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                                                                                                                                             Mismatches
                                                                                                                                                                                           14 TRRSMVFARHLREVGDEFRSRHLNSTDDAD 43
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                                                                                                67.7%; Sccilarity 100.0%; Pr
Conservative 0;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, C2lorf80 protein form C.
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Best Local Similarity 100.
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                        Query Match
Best Local Similarity
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TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Attausher R.D., Feingold E.A., Grouse L.H., Derge J.G.,
R. Strausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
R.A. Hopkins R.F., Jordan H., More T., Max S.I., Wang J., Hsieh F.,
Bratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
R. Stepleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,
R.A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
R. Broak S.A., McKernan R.J., Marke J.A.A., Guabarane P.H.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Helton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
R. Halton D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
R. Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
R. Gones S.J., Marra M.A.,
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Straubberg R.; Straubberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC011044; AAH11044.1; -. SEOUENCE 141 AA; 16478 MW; DA7BBSC658A9DBC4 CRC64;
                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                 Length
Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ database:
EMBL; BC064623; AAH64623.1; -.
SEQUENCE 429 AA; 49975 MW; 36A4213D905AFFD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 136; DB 2;
Pred. No. 1.7e-09;
                                                                                                                                                                     DB 2;
                                                                                                                                                                                                  Pred. No. 2e-11;
                                                                                                                                           67.7%; Scor.
100.0%; Pred. No. 2c.
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         236 TRRSMVFARHLREVGDEFRSRHLNSTDDAD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AA
                                                                                                                                                                                                                                                                                                         14 TRRSMVFARHLREVGDEFRSRHLNSTDDAD 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.4%; S
100.0%;
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                                                                                                                                                                                                                                           30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Matches

g

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EXCURNING FROW N.A. (ISOFORM 2).

RA Strausberg R.L., Feingld E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingld E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Signeton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rabey J., Halton B.K., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ratherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Generation and initial analysis of more than 15,000 full-length human man man and manayer and some sonance will analysis of more than 15,000 full-length human man and sonance was a second sonance was a seco
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                       [1]
SEQUENCE FROM N.A. (ISOFORM 1).
SEQUENCE FROM N.A. (Altonarakis S.E., Guipponi M.;
Menzel O., Reymond A., Antonarakis S.E., Guipponi M.;
"C21orf80, a new gene from the 21q22.3 region: using RNAi to get
"C21orf80, a new gene from the 21q22.3. region: using RNAi to get
insight into the function.";
                                                                                                                                                                              Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: Glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA sequences.
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                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
                           NCBI_TaxID=10090;
  MEDINE=2238257. PubMed=12477932;

XI TISSUE=Brain,

MEDINE=22388257. PubMed=12477932;

XI Strusperg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Altschul M.J., Usdin T.B., Denaldo M.F., Casavant T.L., Scheez T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Yillalon D.K., Muzuy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raticuez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name-Pofut2;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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0
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  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC011044, AAH11044.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11044.1; -.
16478 MW; DA7BB5C658A9D8C4 CRC64;
                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. U.S.A. 99:16899-16903(2002).
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; Pred. No. 1.7e-09;
0; Mismatches 0;
  .;
0
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                                                                                                                                                                                                                                         141 AA
  0; Mismatches
                                                       18 MVFARHLREVGDEFRSRHLNSTDDAD 43
                                                                                                   1 MVFARHLREVGDEFRSRHLNSTDDAD 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 MVFARHLREVGDEFRSRHLNSTDDAD 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVFARHLREVGDEFRSRHLNSTDDAD 26
                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                     14-APR-2004 (TrEMBLrel. 27, 14-APR-2004 (TrEMBLrel. 27, 14-APR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequences.
  Conservative
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                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                     C21orf80 protein.
C21ORF80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
  56;
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RESULT 7
AAH11044
1D 14-P
DT 1

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REQUENCE OF 1-119 FROM N.A.

SEQUENCE OF 1-119 FROM N.A.

SEQUENCE OF 1-119 FROM N.A.

REQUENTEDINIBE_23546831, Dubmed=12466851; DOI=10.1038/nature01266;

RA MEDINIBE_23546831, PubMed=12466851; DOI=10.1038/nature01266;

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Hadka J., Hill D.P., Bulf C., Hume D.A., Chonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bulf C., Hume D.A., Chochashosh J.,

RA Baldarelli R., Farabin A., Matsuda H., Batalov S., Beisel K.W.,

RA Baldar J., A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanai A., Kawaji H., Kawaswa Y., Kedzierski R., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenbard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Ravai T., Need J.C., Reed D.J., Ramachandran S.,

RA Ravai T., Rechaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Shitana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Shitana R., Takenaka T., Konno H., Nakamura M., Sakazume N., Sakazume N., Sato K.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Hashizume W., Imceani K., Tahie Y., Tahie K., Shinagawa A.,

Hara A., Hashizume W., Imceani K., Ishii Y., Itoh M., Kagwa I.,

RA Asunishi A., Soshino M., Waterston R., Lander E.S., Rogers J.,

RA Najazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Namalysis of the mouse transcriptome based on functional annotation of R. Surver 4205-563-57120202.

RA Nature 420.563-5712020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O-glycosidic linkage to a conserved serine or threonine residue in Ear domains (by similarity).

CATALVIIC ACTIVITY: Transfers an alpha-L-fucosyl residue from GDP-beta-L-fucose to the serine hydroxy group of a protein acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catalyzes the reaction that attaches fucose through
roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
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RESULT 8 OFU2 MOUSE

à

OS GENTAL

Isold=Q8VHI3-1; Sequence=Displayed;

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PRT;
                                                                                                                                                                     Protein O-fucosyltransferase 2
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EMBL, AJ575657; CAE02610.1;
Hypothetical protein.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 73.5.
Best Local 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                    01-OCT-2003 (
01-OCT-2003 (
01-MAR-2004 (
                                                                                                                                                                                           Name=pofut2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7TIN6
                                                             Q7YRE5
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Matches
                  RESULT 10
Q7YRE5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
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                                                                                                This SWISS-FROT entry is copyright. It is produced through a collaboration the European the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-linked (GlcNac. .) (Potential).
Wlinked (GlcNac. .) (Potential).
N-linked (GlcNac. .) (Potential).
IGTSVSTFSFRIHEBREILGLDPKTTYNRFCGDQEKACEQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ι,
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDP-fucose protein O-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THWKIAY -> YWHLCFHIFLSDS (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martinez-Dunker I., Mollicone R., Candelier J.J., Breton C., Oriol A. new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases, and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos tautus (Bovine).
Bukaryota; Metazoa;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                    Isoid=Q8VHI3-2; Sequence=VSP 003815;
Note=No experimental confirmation available;
SIMILARITY: Belongs to the glycosyltransferase family 68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.0%; Score 135; DB 1; Length 429;
larity 83.9%; Pred. No. 7.7e-09;
Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.5%; Score 134; DB 2; Length 429; 90.0%; Pred. No. 1e-08; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                            EMBL; AF455270; AAL65192.1; -.
EMBL; BC018194; -; NOT ANNOTATED_CDS.
EMBL, AK009301; BAB26202.1; -.
MGD; MGI:1931140; BC003494.
Alternative splicing; Fucose metabolism; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP 003835.
0E7AFF5F1CD33560 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ll protein.
429 AA; 49757 MW; 8027B56BDEB02DA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 TRRSMVFAKHLRAVGDEFRSQHLNSTDAADK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 TRRSMVFARHLREVGDEFRSRHLNSTDDADE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 TRRSMVFARHLREVGDEFRSRHLNSTDDAD 43
                                                                                                                                                                                                                                                                                                                                                                                                            Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429 AA; 49429 MW;
                                                                                                                                                                                                                                                                                                                                                                                                            3lycosyltransferase; Signal; SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycobiology 13:1c-5c(2003).
EMBL; AJ575655; CAE02608.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 14) Pypothetical protein futi3. Name=futi3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 90.0
1es 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
VARSPLIC
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martinez-Dunker I., Mollicone R., Candelier J.J., Breton C., Oriol "A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases, and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs.";
                                                                                                                         Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                           Loriol C., Germot A., Dupuy F., Maftah A.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY344582; AAQ02334.1; -...
GO; GO:0016757; F:transferase activity, transferring glycosyl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Match
Local Similarity 90.0%; Pred. No. 1.1e-08;
les 27; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 AA; 44572 MW; F697E4600621291B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycosyltransferase, Transferase.
SEQUENCE 459 AA; 52811 MW; 207ECEFE7D3CF7E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
(TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 TRRSMVFARHLRAVGDEFRSRYLNSTDVAD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
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01-OCT-2004 (TrEMBLrel. 28, Created)
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Mottier, Cadieu, Dreano, Lelaure, Galibert F.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
[2]
                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
  and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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les 16; Conserv
                                                                                                                                                                                                                                                  Local Similarity
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01-OCT-2003 (
01-OCT-2003 (
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Matches
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Q7YZS7
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MEDINES-2388257; PubMed=1247793;

MEDINES-2388257; PubMed=1247793;

MEDINES-2388257; PubMed=1247793;

MARIAN STREWN STREWN
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                                                      Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Takifugu.
                                                                                                                                                                                                                                                                                    "A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs."; (glycobiology 13:1C-5C(2003).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                              Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Martinez-Duncker I., Oriol R., Mollicone R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ781759; CAH03734.1; -
Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 386 AA; 44853 MW; CA80543FC5DB7A1D CRC64;
01-OCT-2004 (TrEMBLrel. 28, Last sequence update) 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.1%; Score 117; DB 2; 73.3%; Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 TRRSMVFAKHLRLIGDNFRATHLNSTDISD 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 TRRSMVFARHLREVGDEFRSRHLNSTDDAD 43
                                        Protein-O-fucosyltransferase 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 73.3 es 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                           SEQUENCE FROM N.A. PubMed=12966037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] =
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                    Oriol R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Martinez-Dunker N.A.

Martinez-Dunker N.A.

Martinez-Dunker N.A.

"A new superfamily of protein-0-fucosyltransferases, alpha2-
fucosyltransferases, and alpha6-fucosyltransferases; phylogeny and
identification of conserved peptide motifs.";

Glycobiology 13:1c-5c(2003).

EMBL, AJ575656; CAE02609.1; -.

Hypothetical protein.

SEQUENCE 434 AA; 50605 MW; D853C746D6EE896C CRC64;
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
                                                                                                                                                                                                                                                                                                     ;
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Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 434;
                                                                                                                                                                                                                                              Length 201;
                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
SEQUENCE FROM N.A.
STRAIN=Mix_FVB/N;
TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                          Strausberg'R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003494; AAH03494.1; -.
MGD; MGI:1933140; BC003494.
SEQUENCE 201 AA; 22901 MW; 66889A53389AD124 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein fut13.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
EG:BACN32011.6 protein.
Name=EG:BACN32011.6;
                                                                                                                                                                                                                                           34.5%; Score 79; DB 2; 83.3%; Pred. No. 0.056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.8%; Score 75; DB 2; 53.3%; Pred. No. 0.42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 RRSMVFADALIKTADQFRSKYLDSDDVRDK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 AA
                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 RRSMVFARHLREVGDEFRSRHLNSTDDADE 44
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                                                                                                                                                                                                                                                                                                                                                           27 VGDEFRSRHLNSTDDADE 44
                                                                                                                                                                                                                                                                                                     15, Conservative
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RA Benos P.;
RA Benos P.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL035632, CABB3644.1.; -.
DR InterPro: IPR001412; tRNN-synt I.
DR PROSITE; PS00178; AA TRNA IRGASE I; UNKNOWN I.
SQ SEQUENCE 423 AA, 48995 MW; 28DD706486B39015 CRC64;
Query Match
Sq. Similarity 53.3%; Score 74; DB 2; Length 423;
Best Local Similarity 53.3%; Pred. No. 0.56;
Matches 16; Conservative 5; Mismatches 9; Indels
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Search completed: November 10, 2004, 13:38:25 Job time : 54.7271 sece This Pogo Blone Misproj

Sequence 1, Appli Sequence 35612, A Sequence 27056, A Sequence 27056, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 30607, A Sequence 3607, A Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 26, Appli Sequence 17, Appli Sequence 26, Appli Sequence 2663, A Sequence 27, Appli Sequence 27, Appli Sequence 2866, A Sequence 2866, A Sequence 27, Appli Sequence 2866, A Sequence 27, Appli Sequence 2866, A Sequence 2876, A November 10, 2004, 12:32:37; Search time 15:544 Seconds (without alignments) 191.991 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. US-10-092-750-30 219 1 GLKLATVAASMDRVPKVTPS.....IARENHEPERLGLNGIAETT 45 Description lssued_Patents AA:*
1: /cgn2_6/ptodata1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata1/laa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata1/laa/PcTUS_COMB.pep:* GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. US-08-840-316-1 US-08-809-523-1 US-08-470-76-1 US-09-470-776-1 US-09-724-475-1 US-09-724-475-1 PCT-US93-08849A-1 PCT-US93-08849A-1 US-09-270-767-35615 US-09-270-767-35615 US-09-270-767-35615 US-09-252-991A-27056 US-09-252-991A-27056 US-09-252-991A-27056 US-09-252-991A-27056 US-09-252-991A-30607 US-09-362-899-3 US-09-362-899-3 US-09-362-899-3 US-09-362-899-3 US-10-023-528-17 US-09-134-000C-4723 US-09-252-991A-25876 US-10-140-002-224 US-09-252-991A-32153 Total number of hits satisfying chosen parameters: 478139 seqs, 66318000 residues SUMMARIES Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 % Query Match Length E Score Title: Perfect score: Scoring table: OM protein Sequence: Searched: Run on: Result No.

30, 30, 1884		Sequence 8009, Ap Sequence 2, Appli	Sequence 1, Appli Patent No. 5221789	Sequence 43792, A Sequence 173, App	4476,	Seguence 203, App Seguence 56844, A	Sequence 36791, A Sequence 52008, A	4709	Sequence 6705, Ap
US-09-171-461-30 US-09-970-711-30 US-09-252-991A-18840	US-09-248-796A-16178 US-09-270-767-42409	US-09-489-039A-8009 US-08-190-204-2	PCT-US93-11110-1 5221789-1	US-09-270-767-43792 US-09-538-092-173	US-09-543-681A-4476	US-08-679-493A-203 US-09-270-767-56844	US-09-270-767-36791 US-09-270-767-52008	US-09-270-767-47090	US-09-328-352-6705
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233	22 22	22.8	22	22	22	22.4	22	22	22
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8 6 0 0 0 m	31 32	EI EI EI 44	3 3	78.	6 M	40	44 24 24	44	45

ALIGNMENTS

US-08-40-316.

US-08-40-316.

US-08-40-316.

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,

APPLICANT: Tearev, Sergei. A., and Robinson, Robin A.

TITLE OF INVENTION: A Patherani Strain Of Hepatitis E And Their

TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines

TITLE OF INVENTION: Use In Diagnostic Methods And Their

TITLE OF INVENTION: Use In Diagnostic Methods And Their

TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines

COUNTY: USE METAL OF THE STANDERS:

ASTRET: NEW YORK

COUNTY: USA

CONFUTE: IN MY YORK

COMPUTE: IN PER COMPATIBLE

COMPUTE: IN PER COMPATIBLE

SOFTWARE: MORDERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,316

FILING DATE: IL-ARE-1997

CLASSIFICATION WINBER: 36,425

FILING DATE: RICHARY WINGER: 36,425

TELECOMMUTICATION WINBER: 36,420

TELECOMMUTICATION WINBER: 36,430

TELECOMMUTICATION WINBER: 36,430 Gaps 11; Query Match

29.5%; Score 64.5; DB 3; Length 1693;
Best Local Similarity 37.3%; Pred. No. 1.6;
Matches 19; Conservative 7; Mismatches 14; Indels 11. US-08-840-316-1

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TOPOLOGY: UNKNOWN
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                                                                                                                                                                                                                                                    NEW YORK
NEW YORK
                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-09-402-776-1
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                                                                                                                                                                                                        RESULT 2
US-08-809-523-1
1/2 Sequence 1, Application US/08809523
5 Patent No. 6207416
7 APPLICANT: Tasrev.
7 APPLICANT: Tasrev.
7 ITILE OF INVENTION: Recombinant Proteins Of
7 ITILE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCES: 107
CORRESPONDENCES: 107
CORRESPONDENCES: 107
CORRESPONDENCES: 108
C
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'S Sequence 1, Application US/08471971
'S Sequence 1, Application US/08471971
'S SEMENAL INFORMATION:
APPLICANT: Trarev, Sergei. A., Emerson,
APPLICANT: Sazanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
                                                           616 GLEVRYVAAGLDHRAVFAPGVSPRSAPGEVTAFCSALYRFNREAQRISLTG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 29.5%; Score 64.5; DB 3; Length 1693; Best Local Similarity 37.3%; Pred. No. 1.6; Matches 19; Conservative 7; Mismatches 14; Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: EMB PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPARE: WGNOPDERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,523
FILING DATE: 28-MAY 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13102
FILING DATE: 03-OCT-1995
FILING DATE: 03-OCT-1994
FILING DATE: 18-SEP-1994
FILING DATE: 18-SEP-1997
1 GLKLATVAASMDR----VPKVTPSSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE DOCKET NUMBER: 2026-40321
TELECOMMUNICATION INFORMATION:
TELEPRAX: (212) 758-4800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1693 AMINO ACID RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS: UNKNOWN
UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
STRANDEDNESS: UNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-809-523-1
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Sequence 1, Application US/09402776
) Sequence 1, Application US/09402776
) Patent No. 645852
) GENERAL INPORMATION:
APPLICANT: Emeron Suzanne U., Purcell, Robert H.,
APPLICANT: Taarev, Sergel. A., and Robinson, Robin A.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS: 111
ADDRESSEBE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MONGAN & FINNEGAN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
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29.5%; Score 64.5; DE
Best Local Similarity 37.3%; Pred. No. 1.6;
Matches 19; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2026-4032US2
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: 18M FC COMPATIBLE
COMPUTER: 06-UN-1995
CLASSIFICATION NUMBER: US/08/411,971
FILING DATE: 03-OCT-1994
CLASSIFICATION 1435
FILING DATE: 18-SEP-1992
CLASSIFICATION NUMBER: US/07/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION NUMBER: 2026-4032US
FILING DATE: 18-SEP-1992
CLASSIFICATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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COUNTER READBLE FORM:

ZIF: 10154

COMPUTER READBLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA: 08/316,765

FILING DATE: 03-OCT-1994

CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/316,765

FILING DATE: 18-SEP-1992

CLASSIFICATION: 435

PTILING DATE: 18-SEP-1992

CLASSIFICATION: 435

REGISTRATION NUMBER: 36,459

REFERENCE/DOCKET NUMBER: 2026-4032US

TELECOMMUNICATION INFORMATION:
TELEBRAX: (212) 751-6849

INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CRARACTERISTICS:
LENGTH: 1693 AMINO ACID RESIDUES
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1693 AMINO ACID RESIDUES
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
US-08-470-246-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08316765
Patent No. 6706873
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIN:
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NEW YC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-316-765-1
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APPLICANT: Taarev, Sergei. A., Emerson,
APPLICANT: Taarev, Sergei. A., Emerson,
APPLICANT: Taarev, Sergei. A., Emerson,
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAM & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GLKLATVAASMDR----VPKVTPSSA-----ISSIARENHEPERLGLNG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.5%; Score 64.5; DB 4; Length 1693; Best Local Similarity 37.3%; Pred. No. 1.6; Matches 19; Conservative 7; Mismatches 14; Indels 11
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,246
FILING DATE: 06-UUN-1995
CLASSIPETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/316,765
FILING DATE: 03-COT-1994
CLASSIPETCATION NUMBER: US/07/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION NUMBER: US/07/947,263
FILING DATE: US/07/947,263
FILING DATE: US/07/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION NUMBER: US/07/947,263
FILING DATE: US/07/947,26
                                                                                             PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDBER:
11110G DATE: 11-APR-1997
ATTORNEY/AGENT INPORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4255
TELECOMMUNICATION INFORMATION:
TELEPRAM: (212) 758-4800
TELEFAX: (212) 758-4800
TELEFAX: (212) 758-4800
TELEFAX: (212) 758-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1693 AMINO ACID RESIDUES
TYPE: AMINO ACID
STRANDENES: UNRNOWN
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,776
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08470246
Patent No. 6696242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOPOLOGY: UNKNOWN
US-09-402-776-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10154
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Gaps Query Match 29.5%; Score 64.5; DB 4; Length 1693; Best Local Similarity 37.3%; Pred. No. 1.6; Matches 19; Conservative 7; Mismatches 14; Indels 11; Gaps APPLICANT: TGAREY, Sergei. A., Emerson,
APPLICANT: Suzame U., Purcell, Robert H.

ITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakisteni Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK 1 GLKLATVAASMDR----VPKVTPSSA-----ISSIARENHEPERLGLNG 40 1 GLKLATVAASMDR----VPKVTPSSA-----ISSIARENHEPERLGLNG 40 11; Query Match 29.5%; Score 64.5; DB 4; Length 1693; Best Local Similarity 37.3%; Pred. No. 1.6; Matches 19; Conservative 7; Mismatches 14; Indels 11.

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COMPUTER NEADLE STATES

COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC_CDS/MS_DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION NUMBER: DCT/US3/08849A
FILING DATE: 17-SEP-1993.
PRIOR APPLICATION NUMBER: US07/947,263
FILING DATE: 18-SEP-1992
APPLICATION NUMBER: 26,728
REPRENEWCHOOKENT INFORMATION:
NAME: William S. Feller
REGISTRATION NUMBER: 26,728
REGISTRATION N
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ZIP: 10154
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: ISM PC COMPATIBLE
COMPUTER: NORDPERFECT 5.1
COMPUTER: "TOTAL MORDPERFECT 5.1
COMPUTER: "TOTAL DATA: ""1993/088/
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17-SEP-1993
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GENERAL INFORMATION:
APPLICANT: Taarev, Sergei A., Emerso APPLICANT: Suzanne U., Purcell, Robe TITLE OF INVENTION: Recombinant Frot TITLE OF INVENTION: A Pakistani Strai TITLE OF INVENTION: Use In Diagnosti. NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN STREET: 1345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-SEP-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/947,263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: BORK, Richard, W.
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 37.3
Matches 19; Conservative
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNKNOWN
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PCT-US93-08849A-1
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                                                                                                                       APPLICANT: Tsarev, Sergei. A., Emerson,
Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
A Pakistani Strain Of Hepatitis E And Their
Use In Diagnostic Methods And Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant Proteins Of
A Pakistani Strain Of Hepatitis E And Their
Use In Diagnostic Methods And Vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFENCE/DOCKET NUMBER: 2026-4032US4
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTATIONAL COMPUTATIONAL COMPUTATIONAL COMPUTATIONAL COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK COMPUTATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPRFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,475
FILING DATE: 28-No. 6787145-2000
PRIOR APPLICATION NUMBER: 08/809,523
FILING DATE: CURROWN
APPLICATION NUMBER: US08/316,765
FILING DATE: 18-SEP-1994
APPLICATION NUMBER: 07/947,263
FILING DATE: 18-SEP-1992
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.5%; Score 64.5; Dilarity 37.3%; Pred. No. 1.6; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1693 AMINO ACID RESIDUES TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9308849A
Sequence 1, Application PC/TUS9308849A
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A Pakistani Strain
TITLE OF INVENTION: A Pakistani Strain
TITLE OF INVENTION: A Pakistani Strain
TITLE OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: ASY PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                           Sequence 1, Application US/09724475 Patent No. 6787145 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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Matches 19; Conserva
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Sergei A., Emerson,
U., Purcell, Robert H.
Recombinant Proteins Of
A Pakistani Strain Of Hepatitis E And Their
Use In Diagnostic Methods And Vaccines
                                                                                                                                              29.5%; Score 64.5; DB 5; Length 1693; 37.3%; Pred. No. 1.6; tive 7; Mismatches 14; Indels 11;
                                                                                                       1 GLKLATVAASMDR----VPKVTPSSA-----ISSIARENHEPERLGLNG 40
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Fatent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICANTION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35615
ILENGTH: 153
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US-09-270-767-50832
US-09-270-767-50832
Sequence 50832, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE REPRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF EQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50832
LENGTH: 153
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28.3%; Score 62; DB 4; Length 153;
Best Local Similarity 35.2%; Pred. No. 0.15;
Matches 19; Conservative 5; Mismatches 14; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                         Query Match 29.5%; Score 64.5; DB 5; Length 1693; Best Local Similarity 37.3%; Pred. No. 1.6; Matches 19; Conservative 7; Mismatches 14; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 28.3%; Score 62; DB 4; Length 153; 1 Similarity 35.2%; Pred. No. 0.15; 19; Conservative 5; Mismatches 14; Indels
SEQUENCE CHARACTERISTICS:
LENGTH: 1693 amino acid residues
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US-09-538-092-1044
; Sequence 1044, Application US/09538092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-50832
                                                             ISS: unknown unknown
                                       TYPE: amino acid
; STRANDEDNESS: unk
; TOPOLOGY: unknown
PCT-US93-08849-1
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US-09-270-767-35615
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NS-09-252-991A-27056

// Sequence 27056, Application US/09252991A

// SEXERAL INFORMATION:

// APPLICANT: Marc J. Rubenfield et al.

// TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

// TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

// TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

// TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

// TITLE OF INVENTION: NUMBER: US/09/252,991A

// CURRENT FILING DATE: 1998-02-18

// PRIOR APPLICATION NUMBER: US 60/094,190

// NUMBER OF SEQ ID NOS: 33142

// SEQ ID NO 27056

// LENGTH: 356
; Patent No. 6753314.
; GENERAL INFORMATION:
APPLICANT: Giot, Loic.
APPLICANT: Giot, Loic.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same;
FILE OF INVENTION Protein-Protein Complexes and Method of Using Same;
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: 2000-03-29
PRIOR PILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: OutraPatSeqFormatter Version 0.9
SEQ ID NO 1044
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Patent No. 6733998
GENERAL INFORMATION:
APPLICANT: Jon S. THORSON
TITLE OF INVENTION: ENCOMMOSPORA ECHINOSPORA GENES
TITLE OF INVENTION: ENCOMMOSPORA ELOSYNNHESIS OF
TITLE OF INVENTION: CALICHEAMICIN AND SELF-RESISTANCE THERETO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P30622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 14; Conserv
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US-09-724-797-62
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APPLICANT: Yarbough, Patrice O
APPLICANT: Bradley, Daniel W
APPLICANT: Bradley, Daniel W
APPLICANT: Rawczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk E
APPLICANT: Fry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: De INVENTION: No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                       25.3%; Score 55.5; DB 4; Length 521; 28.2%; Pred. No. 7.8; tive 13; Mismatches 14; Indels 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS(MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
ATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 TVAASMDRVPKVTPSS-AISSIARENHEPERLGLNGIAE
FILE REFERENCE: 2653-40
CURRENT APPLICATION NUMBER: US/09/724,797
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/111,325
PRIOR FILING DATE: 1998-12-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 62
LENGTH: 521
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-UN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US 07/367,486
16-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08478507
Patent No. 6120988
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.2%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bacteria
US-09-724-797-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94306
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US-08-478-507-7
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Gaps
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                                                                                                                                                                                                                                                                                                  DB 3; Length 1693;
                                                                                                                                                                                                                                                                                               Query Match
24.9%; Score 54.5; DB 3; Length 16
Best Local Similarity 35.3%; Pred. No. 55;
Matches 18; Conservative 7; Mismatches 15; Indels
                                    4600-0183.22
         REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600.
TELECHONICATION INFORMATION:
TELEPHONE: (650) 324-080
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1693 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: amino acid
COCCULE TYPE: protein
US-08-478-507-7
Sholtz, Charles K.
                                                                                                                                                                                                                                                                                                                                                                                                                       . Q
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Search completed: November 10, 2004, 13:44:03 Job time : 16.544 secs

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November 10, 2004, 16:36:12; Search time 48.342 Seconds (without alignments) 328.807 Million cell updates/sec
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1 GLKLATVAASMDRVFKVTPS.....IARENHEPERLGLNGIAETT 45
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1: /cgn2 6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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8: /cgn2 6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2 6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2 6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2 6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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16: /cgn2 6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1566620 seqs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                     US-10-092-750-30
                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ų	V	Ω			Ø		Æ	ρ			Æ	
	30, App	27800,	2962, Ap	190999,	221067,	38253, A	184006,	47653,	120, Ap	184040,	291980,	38059, A	223595,
Description	Sequence 30, Appl	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence
ΩI	US-10-092-750-30	US-10-029-386-27800	US-10-104-047-2962	US-10-437-963-190999	US-10-424-599-221067	US-10-425-114-38253	US-10-437-963-184006	US-10-767-701-47653	US-10-087-192-120	US-10-437-963-184040	US-10-425-115-291980	US-10-425-114-38059	US-10-425-115-223595
0B	14	14	14	16	12	15	16	16	13	16	17	15	11
% Query Match Length	4.5	110	742	2045	488	490	786	121	354	1446	1372	208	276
Query Match	100.0	53.9	43.8	29.7	28.8	28.8	28.3	27.6	27.2	26.9	26.7	26.5	26.5
Score	219	118	96	65	63	63	62	60.5	59.5	59	58.5	58	28
Result No.	-	C)	m	4	ιΩ	9	7	œ	თ	10	11	12	13

equence 469 equence 642 equence 223 equence 113	Sequence 291 Sequence 134 Sequence 107 Sequence 564 Sequence 564	291 201 171 178 178 294	equence 692, Ay equence 2214, Ay equence 117, Ay equence 22288, equence 14536, equence 56832,	duence duence du duence du duence du duence du
5 US-10-282-122A-4696 5 US-10-425-114-64239 7 US-10-425-115-22359 6 US-10-437-963-11276 6 US-10-437-963-11096	7 US-10-425-115-2919 6 US-10-437-963-1348 6 US-10-437-961-1378 6 US-10-781-014-564 6 US-10-437-963-1323	US-09-738-626-59 6 US-10-437-963-2 6 US-10-437-963-1 6 US-10-437-963-1 0 US-09-934-455-2	4 US-10-225-066A-622 5 US-10087-192-11 0S-10087-192-11 0S-09-801-368-106 4 US-10-369-493-2228 4 US-10-156-761-14356 5 US-10-222-722-722-72-72-72-72-72-72-72-72-72-	10-437-963-1128 10-437-963-1128 10-437-963-2034 10-437-963-2034 10-425-115-3413 10-437-963-1434 10-424-599-2228
3671	0.00.00.00.00.00.00.00.00.00.00.00.00.0	7 8 2 1 0 8 2 2 4 6 8	99000000	766 11348 11645 1645 1693 4851
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8 8 8 8 8 7 7 7 7 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1	56 56 56 56 56	. սսսսոս		 4.4. 1.0.000 • • • • • • • • • • • • • • • • •
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ALIGNMENTS

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RESULT 1

US-10-02-750-30

| Sequence 30, Application US/10092750
| Publication No. US20030032157A1
| GENERAL INFORMATION:
| APPLICANT: Hammorid, Philip W. |
| APPLICANT: Wright, March C. |
| FILE REFERENCE: 50036/050002
| CURRENT APPLICATION NUMBER: US/10/092,750 |
| FILE REPERENCE: 50036/050002
| CURRENT APPLICATION NUMBER: US/10/092,750 |
| FRIOR APPLICATION NUMBER: US/10/092,750 |
| FRIOR PRING DATE: 2001-03-08 |
| NUMBER OF SEQ ID NOS: 253 |
| NUMBER OF SEQ ID NOS: 253 |
| SEQ ID NO 30 |
| LENGTH: 45 |
| TYPE: PRT |
| ORGANISM: Homo sapiens |
| US-10-092-750-30 |
| Gaps |
| ALCATAVAASMDEVVEVYPSSAISSIARENHEPERLGINGIAETT 45 |
| HIRITALY ABADDRYPEVYTPSSAISSIARENHEPERLGINGIAETT 45 |
| CLKLATVAASMDRYPEVYTPSSAISSIARENHEPERLGINGIAETT 45 |
| US-10-029-386-27800 |
| Sequence 27800 |
| Publication No. US20030194704A1 |
| SEGNERAL HIPORNATION: |
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APPLICANT: Li, Fing Tries and Molecules and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (5321) B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 190999 LENGTH: 2045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: About Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated Mith
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 29.7%; Score 65; DB 16; Length 2045; Best Local Similarity 40.6%; Pred. No. 19; Matches 13; Conservative 6; Mismatches 13; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.8%; Score 63; DB 15; Length 488; Best Local Similarity 31.8%; Pred. No. 5.7; Matches 14; Conservative 12; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| |||:|:|: | ||::|: | 32 ELCQVAANMERLENVISSTDLSQLASDTTLYDPSNIGLGSWVDT 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_41653C.1.pep
US-10-424-599-221067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_8735C.1.pep
US-10-437-963-190999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1). (2045)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AEIGTSMTSEPEKDPSAAKPCISNKNHEPTRI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 ATVAASMDRVPKVTPSSAISSIARENHEPERL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 221067, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38253, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                              Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-10-424-599-221067
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Harzel, David R.
TITLE OF INVENTION: HARZEL DAVIG R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence-Listing Engine vers: 1.1
SEQ ID NO 27800
TYPE: NO 27800
TYPE: NO 27800
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Pred. No. 0.00021;
7; Mismatches 12; Indels
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Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELLX RESEARCH INSTITUTE
TITLE OF INVERTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: US/10/104,047
PRIOR PELING DATE:
PRIOR FILING DATE:
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO ACO16763.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: SYPESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: SYLSSPROT HIT: P38739, EVALUE 1.30e-01
US-10-029-386-27807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LKLATVAASMDRVPKVTPSSAISSIA 27
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Goo, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.8%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2962
LENGTH: 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Homo sapiens
US-10-104-047-2962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-10-437-963-190999
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DEFLICANT: LA ROYALION;

APPLICANT: LA KOVALIC,

APPLICANT: LA KOVALIC,

APPLICANT: Exou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Brobaluk, Brad

APPLICANT: Brobaluk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53221) B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 184040
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                         Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 354;
                                                                                                                                                                                                                                                                                            2 LKLATVAA-SMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT 45
                                                                                                                                                                                                                                                                                                                             33 LAAAVVAAMPMARAPSMSRSGATSTLARRN--RRLGADALTTTT 75
                                                                                                                                                                                   Score 60.5; DB 16; Length
Pred. No. 2.2;
7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 120, Application US/10087192
| Publication No. US2020182586A1
| GENERAL INFORMATION:
| APPLICANT: MOTILS, David W. APPLICANT: Engelhard, Eric K. TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER. FILE REFERENCE: 52942200122
| CURRENT APPLICATION NUMBER: US/10/087,192
| CURRENT FILING DATE: 2002-03-01
| PRIOR FILING DATE: 2000-12-22
| PRIOR PELICATION NUMBER: US 09/747,377
| PRIOR FILING DATE: 2000-12-22
| PRIOR PELICATION NUMBER: US 09/798,586
| PRIOR FILING DATE: 2000-12-02
| NUMBER OF SEQ ID NOS: 2059
| SOFTWARRE: PastSEQ for Windows Version 4.0
                         TYPE: PRT ORGANISM: Sorghum bicolor PEATURE: PEATURE: OTHER INFORMATION: Clone ID: LIB3476-038-P1-K1-C3.pep US-10-767-701-47653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 MATTSASLKRSPSASSLSSMSSVASSVSRPSRTGL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LATVAASMDRVPKVTPSSAISSIARE-NHEPERLGL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.2%; Score 59.5; D
38.9%; Pred. No. 12;
tive 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 184040, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                      Query Match 27.6%;
Best Local Similarity 40.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.2
Best Local Similarity 38.9
Matches 14; Conservative
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-10-437-963-184040
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US-10-087-192-120
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        LENGTH: 121
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; Sequence 184006, Application US/10437963
; Publication No. US2004012334341
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yongwei
    APPLICANT: Cao, Yongwei
    APPLICANT: Cao, Yongwei
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Brabazuk, Brad
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF SEQ ID NUBBER: US/10/437,963
    CURRENT FILING DATE: 2003-05-14
    NUMBER OF SEQ ID NOS: 204966
    SEQ ID NO 184006

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Publication No. US20040172684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yongwei
ITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 47653
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 38253
LENGTH: 490
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                                                                                                                                                                                                                                                                                                                                              Query Match 28.8%; Score 63; DB 15; Length 490; Best Local Similarity 31.8%; Pred. No. 5.8; Matches 14; Conservative 12; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 28.3%; Score 62; DB 16; Length 78 Local Similarity 37.5%; Pred. No. 15; Conservative 7; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KLATVAASMDRVPKVTPSSAISSIAREN--HEPERLGLNGIAET 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 ELCQVAANMERLENVISSTDLSQLASDTTLYDPSNIGLGSWVDT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_81040C.1.pep
US-10-437-963-184006
                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: LIB3106-102-C2_FLI.pep
US-10-425-114-38253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryza sativa
                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-10-767-701-47653
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ORGANISM: Zea mays
FEATURE:
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APPLICANT:
APPLICANT:
  FEATURE:
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Publication No. US20040214272A1
Fublication No. US20040214272A1
Fublication No. US20040214272A1
FUBLICANT: La ROSA, Thomas J.
APPLICANT: Exou, Yihua
APPLICANT: About Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
SEQ ID NOS: 369326
SEQ ID NOS: 369326
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APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITE OF INVENTION: Dlants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 38059
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                                                                                                                                                            Score 59; DB 16; Length 1446;
Pred. No. 85;
6; Mismatches 14; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
) NAME/KEY: unsure

) LOCATION: (1)...(1446)

OTHER INFORMATION: unsure at all Xaa locations

) FEATURE:

) OTHER INFORMATION: Clone ID: PAT_MRT4530_81071C.1.pep

US-10-437-963-184040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.7%; Score 58.5; DB 17; Best Local Similarity 44.1%; Pred. No. 93; Matches 15; Conservative 5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: MRT4577_29373C.1.pep US-10-425-115-291980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LATVAASMDRVPKVTPSSAISS-IARENHEPERL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(1372)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                 112 AEIGTSTTSEPEKDPSEAKSCLSDKNHEPTRM 143
                                                                                                                                                                                                                                                                     S ATVAASMDRVPKVTPSSAISSIARENHEPERL 36
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                   Query Match
Best Local Similarity 37.5%;
Matches 12; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: unsure
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TITLE OF INVENTION: Plants
TITLE OF INVENTION: 38-21632208
CURRENT FILING DATE: 2003-04-28
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FILE REFERENCE: ELITEA 034A
FILE REFERENCE: ELITEA 034A
CURRENT APPLICATION NUMBER: 60/10/282,122A
PRIOR PELING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-28
PRIOR FILING DATE: 2000-05-28
PRIOR FILING DATE: 2000-05-29
PRIOR PELING DATE: 2000-05-29
                                                                                                                                          Gaps
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                                                                                                                                          12;
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                                                                                  Score 58; DB 15; Length 208;
Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 LKLCTAAASCQRPPQKWDQPGPVAENISPSDACQDIS-QNVPPER 219
                                                                                                                                                                                                                             108 LKLCTAAASCQRPPQKMDQPGPVAENISPSDACQDIS-QNVPPER 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                             2 LKLATVAASMDRVPK------VTPSSAISSIARENHEPER 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LKLATVAASMDRVPK------VTPSSAISSIARENHEPER 35
), OTHER INFORMATION: Clone ID: LIB3069-044-Al_FLI.pep
US-10-425-114-38059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_135507C.1.pep
US-10-425-115-223595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 17;
Pred. No. 14;
5; Mismatches 11
                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46968, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oilsen, Kari
APPLICANT: Oilsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Tawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                  26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 37.8%;
Matches 17; Conservative
                                                        Query Match
Best Local Similarity 37.0.
Loc 17; Conservative
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PRIOR FILING DATE: 2000-09-09
PRIOR PELICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2001-02-09
PRIOR PLILING DATE: 2011-02-09
PRIOR PLILING DATE: 2011-02-09
PRIOR FILING DATE: 2011-02-09
PRIOR FILING DATE: 2011-02-16
PRIOR FILING DATE: 2011-02-16
PRIOR PLILING DATE: 2011-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.5%; Score 58; DB 15; Length 391; 37.8%; Pred. No. 22; Live 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GLKLATVAASMDRVPKVTPSSAISSIARENHEPERL----GLNGIAE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LKLATVAASMDRVPK------VTPSSAISSIARENHEPER 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Line Jingdong
APPLICANT: Line, Jingdong
APPLICANT: Line, Jingdong
APPLICANT: Shou, Yibua
APPLICANT: Screen, Serven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nocleic Acid Molecules and Other Molec
TITLE OF INVENTION: Plants and Uses Thereof for Plant Imp
FILE REFERENCE: 38-21(53313)8
CURRENT FILING DATE: 2003-04-28
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; OTHER INFORMATION: Clone ID: LIB3606-012-B7_FLI.pep
US-10-425-114-64239
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; Sequence 64239, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.5
Best Local Similarity 37.8
Matches 17, Conservative
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ORGANISM: Zea mays
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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November 10, 2004, 12:29:32; Search time 10.0259 Seconds (without alignments) 431.857 Million cell updates/sec using sw model - protein search, protein Run on:

ğ

US-10-092-750-30 219 1 GLKLATVAASMDRVPKVTPS......IARENHEPERLGLNGIAETT 45 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

. 283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	Description	hypo	DNA injection prot	microtubule-vesicl	restin - húman	hypothetical prote	ahydr	nel	ribonuclease T [im	9	probable DNA injec	rog	homeotic protein S	alate	dynamin-related pr	PepA protein - Pse	genome polyprotein	probable copper-tr	hypothetical prote	RING-H2 finger pro	thermosome subunit	hypothetical prote	protein F07A11.6 [ferric transport A		M-related protein	probable K+ transp	4	SMY2 protein - yea	ŭ
SUMMAKIES	ID	730	535635	A43336	822695	AB2384	F83853	T43048	AD0695	S38181	H91032	A85877	803631	JE0327	T50334	T09051	MNWHE	S76487	100568	T51854	D84359	T20532	E88320	C71645	F69880	F72346	H71314	694	745	265
	DB																										~			
	Length	147	471	1392	1427	100	1146	1911	215	1169	378	378	413	903	903	687	1693	780	1567	375	959	2722	2738	233	282	304	466	563	790	868
d¥.	Query	97.3	28.3	28.1	28.1	26.9	26.9	26.0	25.6	25.3	25.1	25.1	25.1	25.1	25.1	24.9	24.9	24.7	24.7	24.4	24.4	24.0	24.0	23.7	23.7	23.7	23.7	23.7	23.7	23.7
	Score	213	62	61.5	1.	53	5 0 0	57	56	55.5	55	55	5	55	55	٠	4.	54	54	ω.	53.5	ď	ĸ.	52	52	52	52	52	52	52
	Result No.	-1	7	m	4	Ŋ	9	7	æ	0	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	bifunctional beta-	glutamate synthase	ribonuclease T (EC	RNase T [imported]	RNase T, degrades	hypothetical prote	acetyl-CoA acetylt	acetolactate synth	hypothetical prote	transporter, AcrB/	conserved hypothet	hypothetical prote	methyl-accepting c	related to protein	microtubule-associ
T34488	825322	T06228	A45065	A90924	E85772	D70656	D82429	A82375	T40290	F82159	E87002	A84330	F82383	T51911	A43359
N	_	~	~	~	7	0	C)	N	N	N	~	N	a	0	~
378	006	1023	215	215	215	392	401	548	963	1016	92	450	770	776	2774
23.5	23.5	23.5	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.1	23.1	23.1	23.1	23.1
51.5	51.5	51.5	51	51	51	51	51	51	51	51	50.5	50.5	50.5	50.5	50.5

ALIGNMENTS

	RESULT 1 117303 T17303 T17304 T17304 T17305 C;Species: Homo sapiens (man) 220124.1 - human (fragment)
	Cidate: 12-001-1299 #sequence_revision 13-001-1399 #text_change 07-011-2001 Cidacession: T17303 Ribloccker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
	A; Accession: T17303 A; Accession: T17303 A; Status: preliminary A; Molecule type: mRNA A; Post dine: 1.147 FRIO.
•	A;Cross-references: UNIPROT:Q9UFM9; EMBL:AL117558 A;Experimental source: fetal kidney; clone DKFZp566F2124 C;Genetics: A;Note: DKFZp566F2124.1
	Query Match 97.3%; Score 213; DB 2; Length 147; Best Local Similarity 100.0%; Pred. No. 1.4e-21; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	Oy 2 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT 45

DNA injection protein - phage P22

Ny Alternate names: gp20 protein

C; Species: phage P22

Nucleic Acids Res. 21, 1499; 1993

Nucleic Acids Res. 21, 1499; 1993

A; Title: Sequence of a DNA injection gene from Salmonella typhimurium phage P22.

A; Reference number: S35635; MUID:93219140; PMID:8464750

A; Residues: 1-471 < ADH>
A; Residues: 1-471 < ADH>
A; Residues: 1-471 < ADH>
A; Cross-references: UNIPROT:001076; EMBL:L07556; NID:g215274; PIDN:AAA62407.1; PID:g21527

A; Reference number: A43330; MUID:92394890; PMID:1522065

A; Contents: Salmonella typhimurium

A; Accession: D43330

A; Accession: D43330

A; Accession: D43330

A; Molecula typhimurium

A; Molecula typeliminary

A; Molecula typhimurium

A; Molec

A;Molecule type: DNA A;Residues: 1-92 <CON> A;Cross-references: GB:M93985; NID:g215283; PIDN:AAA72116.1; PID:g215286

N

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Gaps

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A,Molecule_type: DNA_A,Residues: 1-100 <KUR>
A,Residues: 1-100 <KUR>
A,Residues: 1-100 <KUR>
A,Cross-references: UNIPROT: Q8YNEO; GB: BA000019; PIDN: BAB76325.1; PID: g17133763; GSPDB: GAGeneties: ource: strain PCC 7120
C,Genetics: A,Gene: all4626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
A.JTitle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and & A.Reference number: A83550; WUID:20512582; PMID:11058132
A.Accession: F83853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1146 <STO>
A;Cross-references: UNIPROT:Q9KCE1; GB:AP001512; GB:BA00004; NID:g10174030; PIDN:BAB0534
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calcium channel alpha-1 chain - Cyanea capillata (Species: Cyanea capillata CjSpecies: Cyanea capillata CjSpecies: Cyanea capillata CjDate: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004 (Spacession: T43048 R.Jeziorski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V. A.J. 227302, 22799, 1998 AjTitle: Choming and functional expression of a voltage-gated calcium channel alphal submakerence number: 222300; MUID:98380510; PMID:9712913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-1911 <-JEZZ
A,Cross-references: UNIPROT:002038; EMBL:U93075; NID:g1947095; PID:g1947096; PIDN:AAC6308; C,Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C,Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -methyltetrahydrofolate S-homocysteine methyltransferase meth [imported] - Bacillus halc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C.Accession: F93853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: metH
C;Superfamily: cobalamin-dependent methionine synthase; cobalamin-binding
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Conservative 9. v.-
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                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                40
                                                                                                                                                                                                                                                                                                                                                                                          16 AQVNDTPQVSQASATTNAPTATQSIPPERLGLNG 49
                                                                                                                                                                                                                                             Match 26.9%; Score 59; DB 2; Local Similarity 41.2%; Pred. No. 0.92; les 14; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                             9 ASMDRVPKVTPSSAISS -- IARENHEPERLGLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.9%; Score 59; DB 46.2%; Pred. No. 17; iive 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    748 KVTSNELIEAVAREN--PDAIGLSGL 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 KVTPSSAISSIARENHEPERLGLNGI 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 46.2%
Matches 12; Conservative
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nes 11; Conserv
A;Accession: AB2384
A;Status: preliminary
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                                                                                                                                                                                                                                                   Query Match
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Matches
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T43048
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C;Species: Homo sapiens (man)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: 522695; S19853
K;Bilbe, G.; Delabie, J.; Brueggen, J.; Richener, H.; Asselbergs, F.A.M.; Cerletti, N.;
EMBO J. 11, 2103-2113, 1992
A;Title: Restin: a novel intermediate filament-associated protein highly expressed in the A;Reference number: S22695; MUID:92289675; PMID:1600942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB2384.
AB2384.
AB2384.
AB2384.
AB2384.
Associated protein all4626 [imported] - Nostoc sp. (strain PCC 7120)
C)Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C,Accession: AB2384
B, Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Reaidues: 1-1427 <BIL>
A;Cross-references: UNIFROT:P30622; EMBL:X64838; NID:g35998; FIDN:CAA46050.1; PID:g35999
C;Keywords: cytoskeleton
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                                                                                                                                                                                                                                                                                                                                                    crotubule-vesicle linker CLIP-170 - human
Species: Homo sapiens (man)
Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
                                                                                                               Gaps
A;Note: sequence extracted from NCBI backbone (NCBIN:113001, NCBIP:113005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-1392 <PIE>
A;Cross-references: GB:M97501; NID:g180621; PIDN:AAA35693.1; PID:g180622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 1427;
                                                       Score 62; DB 2; Length 471;
Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         C'Accession: A43336
Rapleire, P., Scheel, J.; Rickard, J.E.; Kreis, T.E.
Cell 70, 887-900, 1992
A;Title: CLIP-170 links endocytic vesicles to microtubules.
A;Reference number: A43336; MUID:92405160; PMID:1356075
A;Accession: A43336.
                                                                                                                                                                                                       14 LAGIGAQNENAPKARDINATLGLIRENNDLARSGANNVALT 54
                                                                                                                                                                 4 LATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAET 44
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                                                                                                      7; Mismatches
                                                       28.3%;
                                                                                                            Conservative
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Matches 16; Conservative
                                                                               Best Local Similarity
Matches 14; Conserv
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les 16; Conserv
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                                                       Query Match
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homology

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Gaps

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Gaps

Gaps

us-10-092-750-30.rpr

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A;Molecule type: DNA
A;Residues: 1-378 <HAY>
A;Residues: 1-378 <HAY>
A;Cross-references: UNIPROT:Q8XCM8; GB:BA000007; PIDN:BAB36655.1; PID:g13362702; GSPDB:G:
A;Exross-references: uniprof: gubstrain RIMD 0509952
C;Genetics:
A;Gene: EC83232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homeofic protein Scr - fruit fly (Drosophila melanogaster)
NyAlternate names: sex combs reduced protein
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cipacesion: 803631
R;LeMotte, P.K.; Kuroiwa, A.; Fessler, L.I.; Gehring, W.J.
R;LeMotte, P.K.; Kuroiwa, A.; Fessler, L.I.; Gehring, W.J.
A;Title: The homeotic gene sex combs reduced of Drosophila: gene structure and embryonic
A;Reference number: 803631; MUID:89231621; PMID:2565809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable prophage DNA injection protein 23614 [imported] - Escherichia coli (strain O157 C; Species: Escherichia coli (cjpate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C; Cpate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C; Accession. N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A; A; Litle: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:08XCM8; GB:AE005174; NID:g12516716; PIDN:AAG57477.1; GSPDB:Cl
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Cross-references: FlyBase:FBgm0003339
C;Superfamily: homeobox homeobox homeobox homeobox
C;Reywords: DNA binding; homeobox, nucleus; transcription regulation
F;321-377/Domain: homeobox homeology cHOX.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 2; Length 378;
Pred. No. 16;
5; Mismatches 20; Indels
                                                                                                                                                                                                   2; Length 378,
                                                                                                                                                                                                                                                               20; Indels
                                                                                                                                                                                                                                                                                                                           41
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                                                                                                                                                                                                                                                                                                                                                           14 LAGIGGONSNAPKASDVSEALAYIRONNEMERSGRNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGI
                                                                                                                                                                                                                                                                                                                     4 LATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGI
                                                                                                                                                                                                   Score 55; DB 2
Pred. No. 16;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-413 <LEM>
A;Cross-references: UNIPROT:P09077; EMBL:X14475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 ASMDRVPKVTPSSAISSIARE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 25.1%;
Local Similarity 34.2%;
hes 13; Conservative
                                                                                                                                                                                                   tch 25.1%;
al Similarity 34.2%;
13; Conservative
                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: S03631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: Z3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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$38181
flocculation protein FLO1 homolog YKR102w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: 338181
R;Gaillon, D.; Dujon, B.
submitted to the Protein Sequence Database, March 1994
A;Recence number: 838175
A;Recerence number: 838175
A;Recerence number: 838175
A;Recerence 1-1169 cAAI>
A;Recerence 1-1169 cAAI>
A;Recerence strain $288C
C;Genetics: C;Genetics:
A;Goss-references: SGD:S0001810; MIPS:YKR102w
A;Gone: SGD:FLO10
A;Cross-references: SGD:S0001810; MIPS:YKR102w
A;Map position: 11R
               RESULT 8
AD0655
AD0656
AD0656
AD0656
AD0656
AD06505
AD0605
AD0605
Fibonoclase T [imported] - Salmonella enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AD0695
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quali, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serow A;Reference number: AB0695
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-215 cPAR>
A;Crossion: AD0695
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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H91032
Pyrobable DNA injection protein [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Bscherichia coli
C; Species: Bscherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C; Accession: H91032
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genchapterence number: A99629; MUID:21156231; PMID:11258796
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
25.6%; Score 56; DB 2; Length 215
Best Local Similarity 31.8%; Pred. No. 5.8;
Matches 14; Conservative 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
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48.3%; Pred. No. 51;
:ive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 48.3
Matches 14; Conservative
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4 LATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIA
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                                                                                                                                    dynamin-related protein MSP1 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: 16-Unl-1999 #sequence_revision 16-Unl-1999 #text_change 09-Unl-2004
C;Accession, U.; Belenguer, P.; Menon, Y.; Ducommun, B.
B;Pelloquin, L.; Belenguer, P.; Menon, Y.; Ducommun, B.
Biochem. Biophys. Res. Commun. 251, 720-726, 1998
A;Fitle: Identification of a fission yeast dynamin-related protein involved in mitochond A;Reference number: UE0327; MUID:99008891; PMID:9790976
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-903 <PEL>
A;Cross-references: UNIPROT:P87320; GB:Y07891; NID:g2231081; PIDN:CAA69196.1; PID:g22310
C;Gene: MSP1
A;Gene: MSP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-903 acms
A;Residues: 1-903 acms
A;Residues: 1-903 acms
A;Cross-references: UNIPROT:PB7320; EMBL;AL157874; PIDN:CAB75996.1; GSPDB:GN00067; SPDB:A;Experimental source: strain 972h(-); cosmid c1718
A;Experimental source: strain 972h(-); cosmid c1718
A;Genee: SPDB:SPBC1718.06
A;Map position: 2
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T09051
PepA brottein - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: I--un-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09051
R;Hauser, A.R.; Kang, P.J.; Engel, J.N.
R;Hauser, A.R.; Kang, P.J.; Engel, J.N.
A) Michaer Spa, a secreted protein of Pseudomonas aeruginosa is necessary for cytotoxicit
A;Reference number: Z16536; MUID:98175457; PMID:9515706
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C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D. submitted to the EMBL Data Library, February 2000
A;Reference number: Z25062
STRDISPKLSPSSVVESVARSLNKGVLGGSLAAALPRRFEQQPQRIG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55, DB 2; Length 903;
Pred. No. 44;
3; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 903; 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | : | | | | | | GLRIIGWVTKMDLVP---PSKAI-SILHNNNYPLHYGXIGV 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGI 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GLKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGI 41
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A;Molecule type: DNA
A;Residues: 1-687 <HAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55; DB 2
Pred. No. 44;
3; Mismatches
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ilarity 41.5%;
Conservative 3
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25.1%;
Best Local Similarity 41.5%;
Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserv
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Gaps
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                                                                                Length 687;
                                                                                                              Indels
                                                                              Score 54.5; DB 2;
Pred. No. 37;
5; Mismatches 18;
A, Experimental source: strain PA103
C, Genetics:
A, Gene: pepA
C, Keywords: virulence factor
                                                                                Query Match
Best Local Similarity 38.5%;
Matches 15; Conservative
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42 43

6 LGATASSLNQEPVETPSQAAHKSASLRQEPSGGGL-GVA

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 10, 2004, 12:27:34 ; Search time 54:9482 Seconds (without alignments) 471.205 Million cell updates/sec

Run on:

US-10-092-750-30 219 1 GLKLATVAASMDRVPKVTPS.....IARENHEPERLGLNGIAETT Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 Total number of hits satisfying chosen parameters:

1825181 segs, 575374646 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

SUMMARIES

Q7seg1 neurospora P3344 hepatitis e 08134 hepatitis e 081876 hepatitis e 08444 hepatitis e 08946 hepatitis e 07076 bacteriopha 077487 bacteriopha Am81396 bacteriopha Q9ufm9 homo sapien Q9nut8 homo sapien Q719j1 homo sapien Q96rr7 homo sapien 980y70 mus musculu 980y70 mus musculu 980y14 mus musculu 980d19 xenopus tro 97zuk6 brachydanio 98naq4 homo sapien 99srr6 homo sapien 99srr6 homo sapien 99srr6 homo sapien 99srr6 mus musculu 98c9x6 mus musculu 98c9x6 mus musculu 98c9x6 mus musculu 98c9x8 mus musculu 976n14 salmonella Bad15223 salmonell kenopus tro
brachydanio
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
mus musculu
homo sapien O6p5z9 homo sapien Aah62543 homo sapi P30622 homo sapien Description 2 Q81862 2 Q81876 3 Q89444 2 Q80406 VG20 BPP22 Q77087 Q76H14 BAD15223 Q7SEG1 POLN HEVPA Q81344 Q6P5Z9 AAH62543 REST_HUMAN AAM81396 099NUT8 07L9J1 096RR7 0880Y70 080C14 060C14 060C14 091T77 096RR6 096RR6 095Z299 Q9UFM9 % Query Match Length DB 684 1693 1693 1693 1693 1693 471 Result Š.

Q9ayz0 bacteriopha	Q86wu4 homo sapien	Q9jk25 rattus norv	P79038 emericella	Q6pia3 homo sapien	Aah39081 homo sapi	Q7q4s6 anopheles g	Q8yne0 anabaena sp	Q52407 pseudomonas		Q9kcel bacillus ha	Q75lt9 oryza sativ	Aar00629 oryza sat	Q87qg2 vibrio para
Q9AYZ0	Q86WU4	Q9JK25	P79038	QGPIA3	AAH39081	Q7Q4S6	QBYNEO	Q52407	087058	Q9KCE1	075LT9	AAR00629	0870G2
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449	449	1320	94	350	350	413	100	422	453	1146	1445	1445	310
27.9	27.6	27.6	27.4	27.2	27.2	27.2	26.9	26.9	26.9	26.9	26.9	26.9	26.7
	60.5	60.5	9	59.5	59.5	59.5	23	29	59	23	59	53	58.5
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ALIGNMENTS

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Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

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RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

Antakami K., Yasuda T., Mayanagi T., Wagastsuma M., Shizatori A.,

Rabashi M., Kanda K., Kodaira H., Kondo H., Sugawara M.,

Rabashi M., Kamihara K., Kateuta N., Sato K., Tanikawa M., Yamazaki M.,

An De K., Kamihara M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

Annomiya K., Ishibashi T., Yamashita H., Murakawa M., Pujimori K.,

Rabashin S., Maranabe M., Hiraoka S., Chiba Y., Ishida S.,

Annowiya K., Ishibashi T., Yakeuchi K., Arita M., Inose N.,

Ranachori K., Takahashi-Fuji A., Hara H., Tanase T., Nomura Y.,

Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,

Antashino K., Yuuki H., Oshima A., Sasaki M., Anta M., Sano S.,

Noshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

Noshikawa Y., Matsunawa H., Isthina T., Shiohata N., Sano S.,

Noshikawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

Hishigaki H., Watanabe K., Kumagai A., Takemoto M., Rawakami B.,

Yamazaki M., Matanabe K., Kumagai A., Takemoto M., Pujimori Y.,

Rujimori Y., Xomiyama M., Tashiro H., Takana S., Pukuzumi Y.,

Rujimori Y., Nawajama Y., Noguchi S., Itoh T., Shigata K., Senba T.,

Antunima S., Mata H., Watanabe M., Komatsu T.,

Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

Matsumura K., Nadajima Y., Mizuno T., Morinaga M., Sugano S.,

Nakai K., Yada T., Noguchi S., Itoh T., Shigata K.,

Matsumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

Nakai K., Yada T., Nomura N., Kikuchi H., Masuho S.,

Nomura K., Nagase T., Ohara O., Isogai T., Sugano S.,

Complete sequencing and characterization of 21,243 full-length human
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EQUENCE FROM N.A.

Pubmed=14702039;

Nakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

Nakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

Yamamcto J., Satio K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

Yamamcto J., Satio K., Nawai Y., Isono Y., Nakamura Y., Nagahari K.,

Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

Audo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Kanda K., Yatsuta N., Sato K., Tanikawa M., Yamazaki M.,

Abe K., Kanihara K., Yatsuta N., Sato K., Tanikawa M., Yamazaki M.,

Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

Tanai H., Kimata M., Watanabe S., Yosaida M., Hotuta T., Kusano J.,

An Calya S., Komai F., Hara R., Takahuchi K., Arita M., Imose N.,

Togiya S., Komai F., Hara R., Takahuchi K., Arita M., Imose N.,

Musashino K., Yuuki H., Oshima A., Saaski N., Aotsuka S.,

Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF06752; E Pc_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7L9J1;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ10571.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nat. Genet. 36:40-45(2004).
EMBL, AKO02010; BAA92032.1; -.
InterPro; IPR009607; E.Pc.C.
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AC 07119
AC 07119
DT 05-J
DT 05-J
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     RA Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizur F., Wakebe H., Rhangaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., A Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., A Yamazaki M., Watanabe K., Kunagai A., Takemoto M., Kawakami Y., Ra Duo T., Yamada K., Fujixo M., Injami A., Fujiwara T., Rawakami T., Ozaki K., Hirao M., Ohmori Y., Xomiyama M., Tabinto H., Ikema Y., Okamoto S., A Kawakami T., Nogatake N., Ingagaki H., Ikema Y., Okamoto S., A Okitani R., Kawakami T., Nogatake N., Ingagaki H., Ikema K., Senba T., A Togashi T., Oyama M., Hara H., Watanabe M., Komatsu T., Angashi T., Oyama M., Bata H., Watanabe M., Komatsu T., Autushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Newura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; Tonnal Complete sequenting and characterization of 21,243 full-length human
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Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            627 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                714 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT 757
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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EMBL; AK001433; BAA91688.1; -.

Interpro; IPR009607; EPC.

Pfam; PF06752; E PC. C; 1.

SEQUENCE 676 AA; -75772 NW; 5FCA4646052C0E79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF06752; E Pc C; 1. -
SEQUENCE 763 AA; 86267 MW; B98FCEA0987F7AA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q80Y70;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUAR-2004 (TrEMBLrel. 26, Last annotation update)
D2Ertd694e protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          ch 97.3%; Score 213; DB 2; I
1 Similarity 100.0%; Pred. No. 2.8e-19;
44; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 213; DB 2; I
Pred. No. 3.2e-19;
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100.0%; Pred. No. 3...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
Enhancer of polycomb 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=EPC2;
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Q96RR7
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280Y70
AC Q80Y
DT 01-J
DT 01-J
DT 01-J
DE D2E-M
DB D2E-M
DB D2E-M
CS MUS COC MAMME
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Aziawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aziawa K., Akimura T., Hara A., Hashizume W.,
Rukuda S., Furuno M., Hanagaki T., Haracka T., Hirzoka T., Hirzoka T.,
Hayashida K., Hayatsu N., Hiramoto K., Hirzoka T., Hirzokane T.,
Ratch H., Kawai J., Kolima Y., Rondo S., Konno H., Kouda M., Koya S.,
Katch H., Kawai J., Kolima Y., Rondo S., Konno H., Kouda M., Koya S.,
Katch H., Rawai J., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Sano H.,
Sato R., Saitoh H., Sakazume N., Sano H.,
A sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Togama A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki T.,
Sumitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO47947, BAC3197.1;
BENDI, AKO47947, RPC31197.1;
RIPROSECT R. PC C.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/61; TISSUE=Head;
MFDL/NET=20499374; PubMed=11042159;
MFDL/NET=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-GCYBL/GG; TISSUE-Head;
MEDLINE-COFBL/GG; TISSUE-Head;
A Shibera K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibera K., Itoh M., Aizawa K., Kiteunai T., Tashiro H., Itoh M.,
A Konno H., Akiyama J., Nahah K., Kiteunai T., Tashiro H., Itoh M.,
A Wamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Harada A.,
A Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watehiki M.,
A Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male thymus cDNA, RIKEN full-length enriched
library, clone:5830499114 product:ENHANCER OF POLYCOMB 1 homolog.
Name=DZErtd694e;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 96.3%; Score 211; DB 2; Length 784; Best Local Similarity 97.7%; Pred. No. 6e-19; Matches 43; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pc C; 1.
(: 88272 MW; 761FEEEC6F8BC47B CRC64;
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                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
The FANTOM Consortium,
                                                                                                                                                                                    60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Nature 409:685-690 (2001).
[3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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SEQUENCE 784 AA
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Q8C014
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Colon;

KIALINE=228825; PubMed=1247932;

Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhate N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,

Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toophiyuki S., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodesgren B.J., Lu K., Gibbs R.A.,

Richards S., Worley V.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Villalon D.K., Marny D.M., Sodesgren B.J., Lu K., Gibbs R.A.,

Richards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Schwutz D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

and mouse Anna seconds "...

"Generation and initial analysis of more than 15,000 full-length human
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone:Cl30023C07 product:ENHANCER OF POLYCOMB 1 homolog.
Name=D2Ertd694e;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.3%; Score 211; DB 2;
97.7%; Pred. No. 5.5e-19;
ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CS7BL/60; TiSSUE=Head;
MEDLINE=99279273; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:127721; D2Ertd694e.
InterPro; IPR009607; E.Pc.C.
Pfam; PF06752; E.Pc.C.
NON TER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE PROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
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SEQUENCE
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Query Match
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SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Indtani Y., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Hori F., Indtani Y., Kojima Y., Kondo S., Konno H., Kowda M.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kowda M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J; TISSUB=Thymus; MEDININE-2019374; PubMed=11042159; Carning: P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C7SBL64; FIBLU6861;
SHAIN=C7SBL64; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashinc H., Itoh M.,
Yamamoto H., Akiyama J., Nakamura S., Hazawa M., Nishinc H., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yoneda Y., Ishikawa T., Togawa Y., Izawa M., Ohara B., Watchiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKEN integrateda Sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                           STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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1: _90987 MW; C11D11768C471DDB CRC64;
                                                                                                  Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1277221; D2Ertd694e.
InterPro; IPR009607; E_Pc_C.
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                                                                                                                                                                SEQUENCE FROM N.A.
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Pfam; PF06752;
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Straubberg R.L., Feinged E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
An point R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
As papleron M., Soarsa M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcina A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,
A Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Nones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
Johns S.J., Marra M.A.,
John
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. Second frog) (Silurana tropicalis). Senopus tropicalis (Western clawed frog) (Silurana tropicalis). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibla, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae, Xenopodinae, Xenopodinae, Kenopodinae, Ke
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                                                                                  759 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGLAETT 802
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Submitted (UN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC075105; AAH75105.1; -.
Hypothetical protein:
SEQUENCE 804 AA; 90737 MW; FB320113258FAC2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT
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01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Name=zgc:55784,
Brachydanic rerio (Zebrafish) (Danio rerio).
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MEDLINE=22388257; PubMed=12477932;
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96.3%; Score 211; DB 2; Length 808; 97.7%; Pred. No. 6.2e-19; live 1; Mismatches 0; Indels

Best Local Similarity 97.7 Matches 43; Conservative

Query Match

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=AB: TISSUB=Whole body;

Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,

Astapleton M., Soares M.B., Bonaldo M.F., Casrvinci P., Frange C.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

Jones S.J., Maxer M.A.,

H. Forder E. Handley B. W., Schmitz J., Myers R.M., Schein J.E.,

Jones S.J., Maxer M.A.,

Jones S.J., Maxer M.A.,

H. Mandan A., Smailus D.E., Schmerch A., Schein J.E.,

Jones S.J., Maxer M.A.,

H. Mandan A., Smailus D.E., Schmerch A., Schein J.E.,

H. Mandan A., Schmitz M.J.,

Jones S.J., Maxer M.A.,

H. Marker M. J., Maxer M. J.,

H. Maxer M. J., M
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X PubMed=14702039;

A Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

A Wakamatsu. A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

A Wakamatsu. A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

A Yamamoto J., Sato K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

A Murakami K., Yasuda T., Iwayanagi T., Nodetsuma M., Shiratori A.,

Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

A Takahahi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Cmura Y.,

A Abe K., Kamihara K., Yaki T., Furuya T., Kikkawa M., Yamazaki M.,

Ninomiya K., Ishibashi T., Yamashita H., Murakawa M., Yamazaki M.,

A Tanai H., Kimata M., Matanabe M., Hiraoka S., Chiba Y., Ishida S.,

Ono Y., Takigucini S., Watanabe M., Hara H., Tanase T., Kusano J.,

A Ranehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,

A Togiya S., Komai P., Hara R., Takeuchi K., Arita M., Imose N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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01-MAR-2001 (TYEMBLrel. 16, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
11-MOR-2004 (TYEMBLrel. 26, Last annotation update)
11-MOR-2004 (TYEMBLREL. 26, Last annotation update)
11-MOR-2004 (TYEMBLREL. 26, Last Burnal)
11-MOR-2004 (MORAGA 26, CARTAINT, Hominidee; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703 LKLASVASSLDRVPKVTPTSAI-DIARENHEPERLALNGLSETT 745
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STRAINS-AB; TISSUE-Whole body;
Strausberg R.;
Submitted (RAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC048890; AAH48890.1; -.
InterPro; IPR09607; E. PC_C.
Pfam; PF05722; E. PC_C.
SEQUENCE 751 AĀ; 84613 MW; DIEEC81558F76D04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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NCBI_TaxID=7955;
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2029H7T7
AC
DD O9H7T7
DD O1-MA
DT 01-MA
DD 01-MA
DD 01-MA
DD O1-MA
DD O1-M
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RAMAGRADIO K. VAURIEN, ORDING A. SERRIN N. ACCEPTED S. STRUKE, OF MARGABELO K. VANDERLA S., STRUKE, O. STRUKE, S., VORDING K., MARGADE H., MARGADE K., MARGADE H., MARGADE K., MARGADE H., MARGADE K., MARGADE K., MARGADE H., MARGADE K., MARGADE K.,
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Gaps

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Length 763;

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2 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT 45
MGD, MGI:1278322; Epcl.
Interpro; IRR009607; E.P.C.
Pfam; PF06752; E.P.C.1.
SEQUENCE 763 AA, 84767 MW, D13649721FFB41E2 CRC64;
                                                                                                                   'Match
Local Similarity 52.3%; Pred. No. 0.0011;
les 23; Conservative 7; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA sequences.
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                                                                                                                           Query Match
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ID Q8C9X6
                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                   RESULT 14
Q8NE21
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Matches
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     8 B B B
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Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumira K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The enhancer of polycomb gene of Drosophila encodes a chromatin protein conserved in yeast and mammals.";
Development 125:4052-4066(1998).
EMBL; AF079765; AAC64272.1;
                                                                                                                                                                                                                                                                                                                         ...
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MEDLINE=98407961; PubMed=9735366;
Stankunas K., Berger J., Ruse C., Sinclair D.A., Randazzo F.,
                                                                                                                                                                                                                                                                    43.8%; Score 96; DB 2; Length 742; 52.3%; Pred. No. 0.0011; ive 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 43.8%; Score 96; DB 2; Length 763; 1 Similarity 52.3%; Pred. No. 0.0011; 23; Conservative 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     2 LKLATVAASMDRVPKVTPSSAISSIARENHEPERLGLNGIAETT 45
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Nunes D.N., Dias-Neto E., Brentani R.R., Camargo A.A.;

Nunes D.N., Dias-Neto E., Brentani R.R., Camargo A.A.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; Ar286905; AAK60501.1; -

InterPro; IPR009607; E.Pc.C.

Pfan; PF06752; E.Pc.C.

Pfan; PF06752; E.Pc.C.

Pfan; PF06752; B.Pc.C.

Pfan; PF06752; B.Pc.C.
                                                                                                                                                                                             Pfam; PF06752; E Pc_C, 1. _
SEQUENCE 742 AA; 82701 MW; 54707E36C4F8BF60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      763 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                      Nat. Genet. 36:40-45(2004).
EMBL; AK092304; BAC03857.1; -.
InterPro; IPR009507; E.P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26, Enhancer of polycomb 1.
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                                                                                                                                                                                                                                                                                               Local Similarity 52.3 les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Enhancer of polycomb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Epc1;
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                                                                                                                                                                                                                                                                          Query Match
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                                                                                                 CDNAB.";
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1096RR6
1006RR
AC 096RR
DT 01-DE
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Attaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Appleron M., Soarsa M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Frange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Rodriques S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriquez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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45
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InterPro; IPR009607; E.Pc.C.
Pfam; PF06752; E.Pc.C; 1.—
Pfam; PF06752; E.Pc.C; 1.—
RROUENCE 813 AA; 90893 MW; 1A7DE9D14C291D11 CRC64;
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                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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QBC9X6;
Ol-MAR-2003 (TrEMBLrel. 23, Created)
Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Ol-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 0 day neonate thymus CDNA, RIKEN full-length enriched
library, clone:A430080123 product:enhancer of polycomb homolog 1,
(Drosphila), full insert sequence.

Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxIb=10090;

SEQUENCE FROM N.A.
STRAIN=C57BL/67; TISSUE=Thymus;
MEDLINE=99279283; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).

.. Query Match
43.8%; Score 96; DB 2; Length 813
Best Local Similarity 52.3%; Pred. No. 0.0012;
Matches 23; Conservative 7; Mismatches 12; Indels

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Gaps

Search completed: November 10, 2004, 13:38:28 Job time : 57.9482 secs

SEQUENCE FROM N.A.

GEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

Bukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

Hayashida K., Imotani K., Ishii Y., Itoh M., Kagawa I., Kawakawa T.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,

Katoh H., Kawai J., Kojima Y., Ohno M., Ohsato N., Okazaki Y.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

STRIN=CS7BL/6J; TISSUE=Thymus;

STRIN=CS7BL/6J; TISSUE=Thymus;

STRIN=CS7BL/6J; TISSUE=Thymus;

Shibata K., Itoh M., Aizawa K., Naqaoka S., Sasaki N., Carninci P.,

A Konno H., Akiyama J., Niehi K., Kiteunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

A Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

A Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

A Okazaki Y., Muxamataw T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Nomeda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Nomeda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Sequencing pipeline with 384 multicapillary sequencer.",

Genome Res. 10:1757-1771(2000).

[9]

SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).

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[3] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM CONSOCTIUM,
The FANTOM CONSOCTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I annotation (
"Analysis of the mouse transcriptome based on functional annotation (
60, 770 full-length cDNAs.";
Nature 420:563-573 (2002).

SEQUENCE FROM N.A.
STRAIN=C57BL/60; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM COSOCTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).

Length 813; MGD; MGI:1278322; Epcl. InterPro; IPR09607; B.P.C. Barn; PF06752; B.P.C.1. SEQUENCE 813 AA; 90410 MW; B6F3CD987FC55905 CRC64;

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us-10-092-750-31.rai

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Sequence 434, Appli
Sequence 4141, Appli
Sequence 10, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 316, Appl
Sequence 1146, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 14549, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 11711, A
Sequence 21899, A
Sequence 5782, A A
Sequence 21899, A
                                                                                 November 10, 2004, 12:32:37; Search time 8.981 Seconds (without alignments) 191.991 Million cell updates/sec
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3: /cgr2 & (ptodata/1/laa/5B_COMB.pep:*
4: /cgr2 & (ptodata/1/laa/6A_COMB.pep:*
5: /cgr2 & (ptodata/1/laa/6B_COMB.pep:*
6: /cgr2 & (ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgr2 & (ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-566-076-2

US-09-564-133-4

US-09-248-796A-14141

US-09-507-765-31

US-09-507-765-31

US-09-507-765-31

US-09-507-765-31

US-09-507-765-31

US-09-507-765-31

US-09-507-765-31

US-09-270-767-36676

US-09-270-767-36676

US-09-270-767-36676

US-09-270-767-368-4

US-09-013-598-4

US-09-013-598-4

US-09-013-598-4

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US-09-270-767-3203

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US-09-320-301-303

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US-09-320-301-303

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US-09-320-335-11018
                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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1 MRDLPGHYYETLKFLVGHLKTIADHR 26
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                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
Sequence:
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US-09-270-767-60571	US-09-270-767-45074	US-09-270-767-42487	US-09-507-765-33	US-09-688-188B-15	US-09-291-417D-15	US-08-463-092B-6	US-08-462-109A-6	US-08-460-907B-6	US-08-463-179A-6	US-08-461-384B-6	US-09-513-999C-6835	US-09-513-999C-6836	US-09-513-999C-6837	US-09-107-532A-5869	US-09-710-279-236	US-09-248-796A-17239	US-09-134-001C-4189	
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28	29	30	31	32	33	34	35	36	37	3.8	88	40	41	42	43	44	45	

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RESULT 1

US-09-080-855-2

Sequence 2, Application US/09080855A

Patent No. 6083721

GENERAL INFORMATION:

APPLICANT: Stars, Jan.

APPLICANT: Heldin. Petra

APPLICANT: Heldin. Carl-Henrik

APPLICANT: Heldin. Carl-Henrik

TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1

FILE REFERENCE: L0461/7030

CURRENT APPLICATION NUMBER: US/09/080,855A

CURRENT APPLICATION NUMBER: 08/805,583

EARLIER RILING DATE: 1998-05-18

EARLIER PETRING DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 1261

TYPE: PRI

CREATE PRI

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CREATE PARESH HOMO SapienE
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRDLPGHYYETLKFLVGHLKTIADH 25
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RESULT 2
US-09-566-076-2
US-09-566-076-2
Patent No. 6475775
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sarea, Jan
APPLICANT: APPLICANT: Petra
APPLICANT: APPLICANT: Healman, Ulf
APPLICANT:

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Fri Nov 12 14:55:13 2004

Query Match

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Gaps
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                                                                                                                                                                                                                                                                RESULT 5
PCT-US93-03076-10
| Sequence 10, Application PC/TUS9303076
| GENERAL INFORMATION:
| APPLICANT: Whitehead Institute for Biomedical Research | TITLE OF INVENTION: GAP-Associated Protein p190 and TITLE OF INVENTION: Transduction NUMBER OF SEQUENCES: 20
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: 2 Militia Drive | STREET: 1 Depty disk | COMPUTER READABLE FORM: PC-DOS/MS-DOS | SOFTWARE: PREDABLE FORM: PC-DOS/MS-DOS | SOFTWARE: PREDABLE FORM: PC-DOS/MS-DOS | SOFTWARE: PREDABLE POT/US93/03076 | FLING DATE: 19930331 | STREET: 19930331 | 
                                          10; Indels
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Patent No. 6509155
Sequence 32, Application US/09507765
Sequence 32, Application US/09507765
Sequence 32, Application US/09507765
Sequence 32, Application Tod M.
APPLICANT: Xlinger, Tod M.
APPLICANT: Yue, Henry
APPLICANT: Baughn, Mariah R.
TILLE REFERENCE: PC-0010 US
FILE REFERENCE: PC-0010 US
CURRENT FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PREL PROGRAM
SEQ ID NO 32
LENGTH: 333
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Best Local Similarity 45.5%; Pred. No. 0.84;
Matches 10; Conservative 5; Mismatches
       Best Local Similarity 42.3%; Pred. No. 1.2; Matches 11; Conservative 5; Mismatches
                                                                                                                                                     385 LHSLPVVNFNTLKILVKHLNKISEHK 410
                                                                                                          1 MRDLPGHYYETLKFLVGHLKTIADHR 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI92-03A
TELECOMMUNICATION: 1NFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 LPPAHCETLRYLMAHLKRVTLH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 165 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acid
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PCT-US93-03076-10
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US-09-507-765-32
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Sequence 14141, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: NUCLEIC ACID AND THERAPBUTICS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196 132

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208
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GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Heather
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR
ITILE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE FASTSEQ for Windows Version 3.0
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Best Local Similarity 44.0%; Pred. No. 0.69; Length 1702;
                                                                                                                                                                                                                                                                                                                                                                              9; Indels
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                                                                                                                                                                                                                                                                                                              DB 4;
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EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 IQQLPPPHYRTLEFLMRHLSLLADY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRDLPGHYYETLKFLVGHLKTIADH 25
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Patent No. 6759508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                   TYPE: PRT ORGANISM: Homo sapiens US-09-566-076-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-133-434
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LENGTH: 1702
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Gaps

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Sequence 13446, Application US/09489039A
| General No. 6610836
| General No. 6610836
| TITLE OF INVENTION: NUCENTION: NUCENTE: US/09/489, 039A
| TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REFERENCE: 2709.2004001
| CURRENT APPLICATION NUMBER: US/09/489, 039A
| CURRENT PELIANG DATE: US/00/01-27
| PRIOR FILING DATE: US/00/117,747
| PRIOR FILING DATE: 1999-01-29
| NUMBER OF SEQ ID NOS: 14342
| LENGTH: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36.76. Application US/09270767

Sequence 36.76. Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36676

LENGTH: 142
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; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ϊ,
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35.3%; Score 50.5; DB 4; Length 363;
Best Local Similarity 41.7%; Pred. No. 7.4;
Matches 10; Conservative 7; Mismatches 6; Indels
Query Match 37.1%; Score 53; DB 4; Length 433; Best Local Similarity 39.1%; Pred. No. 3.7; Matches 9; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h Similarity 40.0%; Pred. No. 6.2; 8; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| |::: |:|| | :::|:|
197 MRDQAIHFFDLLRFLTGDEVRTVA 220
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                                                                                                                                                                                                   307 LRSLPEHNYVVLRYLMGFLHAVS 329
                                                                                                                                                        1 MRDLPGHYYETLKFLVGHLKTIA 23
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 PGHYYETLKFLVGHLKTIAD 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-489-039A-13446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-270-767-36676
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                                                                                                                                                                                                                                                                 37.1%; Score 53; DB 4; Length 333; ilarity 39.1%; Pred. No. 2.7; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53; DB 4; Length 433;
Pred. No. 3.7;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6509155 404424.5.pseq
US-09-507-765-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
) OTHER INFORMATION: Incyte ID No. 6509155 3068538CD1
US-09-507-765-30
                                                                              PEATURE:
NAME/KEY: misc feature
J. OTHER INFORMATION: Incyte ID No. 6509155 g6572185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/09507765
Patent No. 6509155
Fatent No. 6509155
FATENT NO. 6509155
FAPLICANT: Ninger, Tod M.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USCOULT,
Sequence 30, Application US/09507765
Sequence 30, Application US/09507765
Sequence 30, Application US/09507765
Sequence 30, Application US/09507765
Sequence 30, Application:
Sewart Triager, Tod M.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Stewart, Elizabeth A.
TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS
TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS
TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS
CURRENT APPLICATION NUMBER: US/09/507,765
NUMBER OF SEQ ID NOS: 33
SOPTWARE: PERL PROGRAM
SEQ ID NO 30
IBRIGH: 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRDLPGHYYETLKFLVGHLKTIA 23
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Best Local Similarity 39.1%;
Matches 9; Conservative 6
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ORGANISM: Homo sapiens
                                                  ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-507-765-31
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Fri Nov 12 14:55:13 2004

RESULT 14

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Gaps
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                                            6; Indels
Query Match
33.2%; Score 47.5; DE
Best Local Similarity 27.3%; Pred. No. 54;
Matches 12; Conservative 5; Mismatches
                                                                                      4 LPGHYYE----TLKF--
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604 LPGSYYKINESMIKFHTENAEDQDRVASVIGDAITHINTVFDHR 647
                                                                                          RESULT 13
US-08-290-301-4
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US-07-841-997A-4
; Sequence 4, Application US/07841997A
; Sequence 4, Application US/07841997A
; Patent No. 542254
; GENERAL INFORMATION:
    APPLICANT: Londesborough, John
    APPLICANT: Londesborough, John
    APPLICANT: Vuorio, Outi
; TITLE OF INVENTION: A method to increase the trehalose content
; TITLE OF INVENTION: A method to increase the trehalose content
; TITLE OF INVENTION: Structural genes for the short and long chains
; TITLE OF INVENTION: yeast trehalose synthase.
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS;
; ADDRESSEE: ALA.
STREET: 1-1-1;
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                     DB 4; Length 142;
                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: Finland

ZIP: SF-0101

ZIP: SF-0101

COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette, 3.5 inch, 720 KD

COMPUTER: IBM PC/XT/AT

OPERATING SYSTEM: PC-DOS

SOFTWARE: WP5.1 file exported as DOS text file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,997A

FILING DATE: 19920228

CLASSIFICATION ADATA:
APPLICATION NUMBER: 07/835,021

FILING DATE: February 14, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Mary E. Gormley

REFERENCE/DOCKET NUMBER: 34409

REFERENCE/DOCKET NUMBER: 3409

REFERENCE/DOCKET NUMBER: 320085A

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                   Query Match
33.6%; Score 48; DB (
Best Local Similarity 40.0%; Pred. No. 6.2;
Matches 8; Conservative 5; Mismatches
CURRENT APPLICATION NUMBER: US/09/270,767 CURRENT FILING DATE: 1999-03-17 NUMBER OF SEQ ID NOS: 62517 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 51893 LENGTH: 142
                                                                                                                                                            ORGANISM: Drosophila melanogaster US-09-270-767-51893
                                                                                                                                                                                                                                                                                                                             5 PGHYYETLKFLVGHLKTIAD 24
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PNHYFDLLLRLLGRLNTLKE 74
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202)659-2930
TELEFAX: (202)887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 785 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AM
TOPOLOGY:
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TELEX: 4
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APPLICANT: Londesborough, John
APPLICANT: Londesborough, John
APPLICANT: Tunnela, Outi
APPLICANT: Tunnela, Outi
APPLICANT: Palva, Tupio
APPLICANT: Welin, Bjorn
APPLICANT: Welin, Bjorn
APPLICANT: Welin, Bjorn
TITLE OF INVENTION: Increasing the trehalose content
TITLE OF INVENTION: of organisms by transforming them with combinations of
TITLE OF INVENTION: the structural genes for trehalose synthasse.
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alko Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC/XTATA

COMPUTER: IBM PC/XTATA

OPERATING SYSTEM: PC-DOS

SOGTWARE: WFS.1 file exported as DOS text file
CURRENT APPLICATION:DATA:
APPLICATION NUMBER: US/08/290,301
FILING DATE: 15 AUGUST 1994

CLASSIFICATION NUMBER: F 1943133
FILING DATE: 29 June 1994
APPLICATION NUMBER: F 1993
APPLICATION NUMBER: PCT/F193/00049
FILING DATE: 15 February 1993
APPLICATION NUMBER: 07/841,997
FILING DATE: 18 February 1992
APPLICATION NUMBER: 07/841,997
FILING DATE: 1995
ATORNEY/AGENT INPORMATION:
NAME: Kubovcik, Ronald J.
NAME: Lydon, James C.
REGISTRATION NUMBER: 25,401
REGISTRATION NUMBER: 25,401
REGISTRATION NUMBER: 30,082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: Finland
ZIP: SF-00101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: LAIN-001
TELECOMMUNICATION INFORMATION:
TELEPRONE: (202) 467-6300
TELEPRAX: (202) 466-2006
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
Sequence 4, Application US/08290301
Patent No. 5792921
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LPGHYYE----TLKF-----
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Amino acid
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FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Alko Ltd.
STREET: PO Box 350
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Helsinki
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APPLICANT: PURDERAY OLLA
APPLICANT: PURSHING: TURNER APPLICANT: PURSHING: APPLICANT: PURSHING: APPLICANT: PURSHING: APPLICANT: PURSHING: APPLICANT: Maid, Abul
TITLE OF INVENTION: Increasing the trehalose content
TITLE OF INVENTION: of organisms by transforming them with combinations of
TITLE OF INVENTION: of organisms by transforming them with combinations of ITTLE OF INVENTION: of organisms by transforming them with combinations of ITTLE OF INVENTION: the structural genes for trehalose synthase.

ADDRESSERS AND LEG
STREET: PO BOX 350
CITY: Helsinki SPETIS PORM:
STREET: PO BOX 350
COMPUTER: THEN PORM: POR
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           Sequence 4, Application US/09013598
Sequence 4, Application US/09013598
Patent No. 6323001
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tunnela, Outi
APPLICANT: Tunnela, Outi
APPLICANT: Holmstrom, Kjell-Ove
APPLICANT: Mandel, Abul
TITLE OF INVENTION: Increasing the trehalose content
TITLE OF INVENTION: of organisms by transforming them with combinations of
TITLE OF INVENTION: the structural genes for trehalose synthase.
NUMBER OF SEQUENCES: 85
CORRESPENDENCE ADDRESS:
ADDRESSEE: Alkolid.
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Pred. No. 54;
5; Mismatches 6; Indels 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Helsinki
STATE:

COMPTRY: Finland
ZIP: SF-00101

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: PC-DOS
SOFTWARE: WFS.1 iille exported as DOS text file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,598
FILING DATE:
TLING DATE: SPENTARY: 08/290,301
APPLICATION NUMBER: PCT/F193/00049
FILING DATE: 15 FEDRUARY: 1993
APPLICATION NUMBER: 07/841,997
FILING DATE: 15 FEDRUARY: 1992
APPLICATION NUMBER: 07/844,997
FILING DATE: 14 FEDRUARY: 1992
APPLICATION NUMBER: 07/846,021
FILING DATE: 14 FEDRUARY: 1992
ATTORNEY/AGENT INFORMATION:
NAME: KUDOVCH, ROHARD: 25,401
REGISTRATION NUMBER: 25,401
REGISTRATION NUMBER: 25,401
REGISTRATION NUMBER: 30,082
REFERENCE/DOCKET NUMBER: 30,083
REFERENCE/DOCKET NUMBER: 30,083
REFERENCE/DOCKET NUMBER: 30,083
REFERENCE/DOCKET NUMBER: 30,083
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 785 amino acids
TYPE: Amino acid
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Best Local Similarity 27.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LPGHYYE----TLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Alko Ltd.
PO Box 350
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21;
Score 47.5; DB 1; Length 1098;
Pred. No. 79;
                                                                                              4 LPGHYYE----TLKF------LVGHLKTIADHR 26
                                         5; Mismatches
                                                                                                                                                            Search completed: November 10, 2004, 13:44:04 Job time : 9.981 secs
       Query Match
Best Local Similarity 27.3%;
Matches 12; Conservative 5
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Sequence 82, Application US/08290301 Patent No. 5792921 GENERAL INFORMATION: APPLICANT: Londesborough, John

RESULT 15 US-08-290-301-82

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1 MRDLPGHYYETLKFLVGHLKTIADHR 26
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Sequence 726, App
Sequence 725, App
Sequence 724, App
Sequence 774, App
Sequence 278, App
Sequence 278, App
Sequence 278, App
Sequence 134, App
Sequence 134, App
Sequence 134, App
Sequence 434, App
Sequence 434, App
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1: /cgn2_6/ptodata/1/pubpaa/BC7_NEW PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-072-012-726

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8 US-10-10-278

8 US-10-10-278

6 US-10-10-10-28

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 56, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 21, Appl
Sequence 32, Appl
Sequence 31, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 28, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 152761,
Sequence 152761,
Sequence 152761,
Sequence 152761,
Sequence 152762,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 26;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence of Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Hammond, Philip W.
; TITLE OF INFORMATION: Polypeptides Interactive with BCL-X1
; TITLE OF INFORMATION: Polypeptides Interactive with BCL-X1
; FILE REPERBNCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; NUMBER OF SEQ ID NOS: 253
; SEQ ID NO 31
: ENGINE 26
; LENGTH: 26
             14 US-10-369-493-1773
14 US-10-265-194-95
15 US-10-108-248-24
15 US-10-108-248-24
15 US-10-108-248-24
15 US-10-108-248-24
18 US-10-108-248-24
19 US-09-802-127-7
19 US-09-802-127-7
14 US-10-284-753-32
14 US-10-284-753-31
14 US-10-284-753-31
15 US-10-097-340-14
16 US-10-097-340-14
17 US-10-097-340-19
18 US-10-097-340-19
18 US-10-097-340-18
18 US-10-424-599-152765
18 US-10-424-599-152765
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18 US-10-424-599-152765
18 US-10-424-599-152765
18 US-10-424-599-152765
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Best Local Similarity 100.0%; Pred. No. 2.9e-14;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                    TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-750-31
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Gaps

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Indels

56

S-10-072-012-726 Sequence 726, Application US/10072012 Publication No. US20040033493A1 GENERAL INFORMATION:

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APPLICANT: Lepley, Denies M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burges, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE BURGES: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT APPLICATION NUMBER: US/265,102
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR PILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR PILING DATE: 2001-02-08
                            Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
Miller, Charles E.
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Furtak, Katarzyna
Grosse, William M.
Alsobrook II, John P.
                                                                                                                                                                                        Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
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Rieger, Daniel K
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                                                                                                          APPLICANT
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APPLICANT: Lepley, Denies M.
APPLICANT: Reger, Catherine E.
TITLE OF INVENTION: Proceeds and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT FILING DATE: 2002-01-31
FRICA PLICATION NUMBER: 60/265,102
PRIOR PLICATION NUMBER: 60/265,514
PRIOR PLICATION NUMBER: 60/265,517
PRIOR PLICATION NUMBER: 60/265,517
PRIOR PLICATION NUMBER: 60/265,412
PRIOR PLICATION NUMBER: 60/266,406
PRIOR PLICATION NUMBER: 60/266,767
PRIOR PLICATION NUMBER: 60/266,77
PRIOR PLICATION NUMBER: 60/267,757
PRIOR PLICATION NUMBER: 60/266,77
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                                                                                                                                                                                                                         Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
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Furtak, Katarzyna
Grosse, William M.
Alsobrook II, John P.
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Wolenc, Adam R.
Patturajan, Meera
                            Shimkets, Richard
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Rieger, Daniel K.
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; ORGANISM: Homo sapiens
US-10-072-012-726
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PRIOR FILING DATE: 2001-02-07
PRIOR PLILING DATE: 2001-02-08
PRIOR PLILING DATE: 2001-02-08
PRIOR PLILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 725
TYPE: PRT
TYPE: PRT
ORGANISM: Homo sapiens
Ouery Match
SEC ID NO 725

I MRDLEGHYVETLKFLVGHLKTIADH 25
Best Local Similarity 64.0%; Pred. No. 9.3e-05; DB 15; Length 1173;
Best Local Similarity 64.0%; Pred. No. 9.3e-06;
Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

ATTPE: PRT
ON 725

APPLICANT: Application US/1015368
PUBlication No. US2003092616A1
Sequence 212, Application US/1015368
PUBLICANT: MATSUDA, Akio
APPLICANT: MATSUDA, RUNA
APPLICANTION: MATSUDA, R
```

5-10-072-012-725
Sequence 725, Application US/10072012
Sequence 725, Application US/10072012
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Serhusen, Bryan

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RESULT 7
US-10-072-012-278
; Sequence 278, Application US/10072012
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CRCANISM: Homo sapiens
US-10-153-668-470
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Homo sapiens
US-10-072-012-724
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APPLICANT: Colman, Carol E. A
APPLICANT: Wolenc, Adam R.
APPLICANT: Furtak, Katarzyna
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Rieger, Danise M.
APPLICANTON: Proteins and Nucleic Acids Encoding Same FILE REFRENCE: 21402-258
CURRENT FLING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR PILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,317
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,317
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

64.3%; Score 92; DB 14; Length 1286;
Best Local Similarity 64.0%; Pred. No. 0.0001;
Matches 16; Conservative 5; Mismatches 4; Indels
CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
PRIOR FILING DATE: 2002-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-06-31
PRIOR FILING DATE: 2001-08-31
PRIOR PILING DATE: 2001-08-31
PRIOR PILING DATE: 2001-08-31
PRIOR PILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR PILING DATE: 2001-06-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-06-25
PRIOR PILING DATE: 2001-06-35
PRIOR PILING DATE: 2001-06-36
PRIOR PILING DATE: 2001-06-36
PRIOR PILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
SOFTWARE: PARCHIN VET: 2.0
SOFTWARE: PARCHIN VET: 2.0
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Publication No. US20040033493A1
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Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
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Patturajan, Meera
Shimkets, Richard
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US-10-153-668-212
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PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/266,767

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-05

PRIOR PAPLICATION NUMBER: 60/266,767

PRIOR APPLICATION NUMBER: 60/266,975

PRIOR APPLICATION NUMBER: 60/266,975

PRIOR APPLICATION NUMBER: 60/266,975

PRIOR APPLICATION NUMBER: 60/267,459

PRIOR PILING DATE: 2001-02-08

PRIOR PILING DATE: 2001-02-08

PROMINING PRIOR APPLICATION NUMBER: 60/267,459

PRIOR PILING DATE: 2.1

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 724

LENGTH: 1266

TYPE: DPT
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64.3%; Score 92; DB 15; Length 1286;
Best Local Similarity 64.0%; Pred. No. 0.0001;
Matches 16; Conservative 5; Mismatches 4; Indels
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64.3%; Score 92; DB 14; Length 1354;
Best Local Similarity 64.0%; Pred. No. 0.00011;
Matches 16; Conservative 5; Mismatches 4; Indels
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APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
APPLICANT: MATSUDA, Akio
APPLICANT: MURAMATEN, Shuji
APPLICANT: INTRAMA, Kenya
TITLE OF INVENTION: STATE Activating Gene
FILE REFERENCE: 1254-0207P
FILE REFERENCE: 1254-0207P
FRICE APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-06-31
PRIOR FILING DATE: 2001-06-31
PRIOR FILING DATE: 2001-06-31
PRIOR FILING DATE: 2001-06-31
PRIOR FILING DATE: 2001-06-35
PRIOR FILING DATE: 2001-06-35
PRIOR FILING DATE: 2001-06-36
PRIOR FILING DATE: 2001-07
PRIOR FILING D
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591 IHDLPEHHYETLKFLSAHLKTVAEN 615
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59.4%; Score 85; DB 14; Length 816; 68.2%; Pred. No. 0.0007; tive 3; Mismatches 4; Indels
TITLE OF INVENTION: No. US20030236392Alel full length cDNA FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zerhusen, Bryan
                                                                                                                                                                                                                                                              15; Conservative
                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-104-047-2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | SEQ ID NO 2
| LENGTH: 1261
| TYPE: PRT
| ORGANISM: Homo sapiens
| US-10-177-980-2
                                                                                                                                                                                                                                        Best Local Similarity
Matches 15; Conserv
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US-10-072-012-733
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                                                                                                                                                                                                                                                                                        APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Furtak, Katarzyna
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Catherine E.
APPLICANT: Burgess, Catherine E.
APPLICANT: Burgess, Catherine E.
APPLICANT: 21402-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : ||| |:|||||| ||||::
659 IHDLPEHHYBTLKFLSAHLKTVAEN 683
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Sequence 2050, Application US/10104047

Publication No. US20030236392A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE
                                                                                                                                                                                             Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
                                                                                                                                               Padigaru, Muralidhara
Anderson, David W.
                              Tchernev, Velizar
Spytek, Kimberly
Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
      No. US20040033493A1
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Wolenc, Adam R.
                                                                                                                                                                                  Rastelli, Luca
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US-10-072-012-278
                                                                                                                                                                                                                                                                          Wolenc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
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APPLICANT: Saras, Jan
APPLICANT: Franch, Petra
APPLICANT: Franch, Petra
APPLICANT: Franch, Pontus
APPLICANT: Hellman, Ulf
APPLICANT: Hellman, Ulf
APPLICANT: Heldin, Carl-Henrik
Gonza, Leonel Jorge
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
TITLE OF INVENTION: US/10/177, 980
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US/9/080, 855
PRIOR FILING DATE: 1999-05-18
PRIOR PELICATION NUMBER: 08/805,583
PRIOR FILING DATE: 1997-02-25
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  Gaps
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRDLPGHYYETLKFLVGHLKTIADH 25
                                                                           1 MRDLPGHYYETLKFLVGHLKTI 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 733, Application US/10072012 Publication No. US20040033493A1 GENERAL INFORMATION:
                                                                                                                                                                                                                       Sequence 2, Application US/10177980 Publication No. US20030166232A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patturajan, Meera
Shimkets, Richard
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PUDLICATION NO. US20020183499A1

GENERAL INFORMATION:

APPLICANT: Lodes, Michael J.

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: Benson, Darin R.

APPLICANT: Benson, Darin R.

TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER;

TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER;

FILE REFERENCE: 210121.475C10

CURRENT APPLICATION NUMBER: US/09/854,133

CURRENT APPLICATION NUMBER: 201-05-11

NUMBER OF SEQ ID NOS: 735

SOFTWARE: FastSEQ for Windows Version 3.0

SERVICE SEQ ID NOS: 735

TYPE: PRT
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                                                                                                                                       DB 16; Length 1261;
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APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: 02/09/138,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587-12-14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 434
LENGTH: 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.4%; Score 62; DB 9; Length 1702;
44.0%; Pred. No. 4.5;
tive 7; Mismatches 7; Indels
                                                                                                                                                                                                    9; Indels
                                                                                                                                          Score 65; DB 1
Pred. No. 1.1;
5; Mismatches
                                                                                                                                                                                                                                                                                             101 IQQLPPPHYRTLEFLMRHLSLLADY 125
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                                                                                                                                                                                                                                                            1 MRDLPGHYYETLKFLVGHLKTIADH 25
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Patent No. US20020110563A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Algate, Paul A.
Secrist, Heather
Indirias, Carol Yoseph
Benson, Darin R.
Elliot, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed, Steven G.
Henderson, Robert A
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
                                                                                                                                          Query Match
Best Local Similarity 44.0%;
Matches 11; Conservative
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Best Local Similarity 44.0
Matches 11; Conservative
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ORGANISM: Homo sapiens
US-09-738-973-434
                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-192
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US-09-854-133-434
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US-09-738-973-434
LENGTH: 1261
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TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REFERENCE: D0273 NP
CURRENT APPLICATION NUMBER: U$/10/648,593
PRIOR FILING DATE: 2003-08-26
PRIOR FILING DATE: 2003-08-27
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
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Best Local Similarity 44.0%; Pred. No. 1.1;
Matches 11; Conservative 5; Mismatches
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CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 06/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR PLING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-05
PRIOR PLING DATE: 2001-02-05
PRIOR PLING DATE: 2001-02-05
PRIOR PLING DATE: 2001-02-05
PRIOR PLING DATE: 2001-02-07
PRIOR PLING DATE: 2001-02-08
Remaining Prior Application data removed - 8
SOFTWARE: PARCENTIN VUMBER: 60/266,975
PRIOR PLING DATE: 2001-02-08
REMAINING PRIOR PRIOR PRIOR PRIOR PLING DATE: 2001-02-08
PRIOR PLING DATE: 2001-02-08
PRIOR PLING DATE: 2001-02-08
PRIOR PLING DATE: 2001-03-08
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Publication No. US20040106132A1
GENERAL INFORMATION:
                        Miller, Charles E. Gerlach, Volerite Taymond J. Gusev, Vladimir Y. Colman, Seven D. Wolenc, Adam R. Pena, Carol E. A.
                                                                                                                                                                                                                          Furtak, Katarzyna
Grose, William M.
Alsobrook II. John P.
Lepley, Denise M.
Rieger, Daniel K.
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SOFTWARE: Patentin version 3.2
SEQ ID NO 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-012-733
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Search completed: November 11, 2004, 01:28:13 Job time : 28.9809 secs
                                                                                                                        Query Match
Best Local Similarity
Matches 11; Conserv
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FULLE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOSTWARE: Patentin version 3.0
SEQ ID NO 56
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APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG
CURRENT FALICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FastSEQ for Windows Version 3.0
INDIGHT: 1702
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                                                                        Query Match 43.4%; Score 62; DB 9; Length 1702; Best Local Similarity 44.0%; Pred. No. 4.5; Matches 11; Conservative 7; Mismatches 7; Indels
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43.4%; Score 62; DB 1
Best Local Similarity 44.0%; Pred. No. 4.5;
Matches 11; Conservative 7; Mismatches
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Royer, John
Salama, Sofie
Sherman, Amir
Silva, Jeff
                                                                                                                                                                                                     101 IQQLPPPHYRTLEFLMRHLSLLADY 125
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Sequence 434, Application US/10144649A
Publication No. US20030118599A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56, Application US/09801368
Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Busby, Robert
Call, Brian
Hecht, Peter
Holtzman, Doug
Madden, Kevin
Maxcon, Mary
Milne, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-649A-434
; ORGANISM: Homo sapiens
US-09-854-133-434
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Gaps
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0
                                                                                    40.6%; Score 58; DB 9; Length 2167; 44.0%; Pred. No. 24;
                                                                                                                        9; Indels
                                                                                                                        5; Mismatches
                                                                                                                                                                               2090 LQKLPTCYYQTLKRIVFHLNKVHQH 2114
                                                                                                                                                         1 MRDLPGHYYETLKFLVGHLKTIADH 25
; LENGTH: 2167
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-388-56
                                                                                                                        11; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 14:52:32 ; Search time 5.12456 Seconds (without alignments) 281.634 Million cell updates/sec Run on:

US-10-092-750-228 86 86 1 TLRHWGLQFNTRFGV 15. Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match.0% Maximum Match 100% Listing first 45 summaries

pIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	equine arteritis	conserved hypothe	branched-chain ami	hypothetical prote	hypothetical prote	-	Ĕ	hypothetical prote	conserved hypothe	hypothetical membr	oug protein - Baci	transporter, FNT	formate-nitrate tr	hypothetical prote	conserved hypothet	alcohol dehydrogen	alcohol dehydrogen	hypothetical prote				agaA protein [impo	protei	hemocyanin chain	probable membrane	irp5 protein - Yer	yersiniabactin sid	
	ID	B40901	T40174	857763	A64143	T26721	A42902	F83198	T23175	D95941	AF3448	JC2302	H95140	H98008	B72226	AF0146	JC1376	H70860	A90016	877009	AE2346	AC2015	T45529	A36861	PL0165	AB1013	T30345	AG0232	
	DB	10	N	N	7	N	N	0	7	N	~	N	N	N	~	~	~	N	N	~	N	N	7	N	N	7	N	~	,
	Query Match Length	540	277	363	98	128	307	307	650	412	417	147	265	265	277	285	346	346	49	275	283	467	509	1463	415	492	525	525	
оko	Query Match	57.0	51.2	51.2	50.0	50.0	50.0	50.0	48.8	48.3	48.3	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.1	46.5	46.5	46.5	46.5	46.5	45.3	45.3	45.3	45.3	
	Score	4.9	44	44	43	43	43	43	42	41.5	41.5	41	41	41	41	41	41	41	40.5	40	40	40	40	40	39	39	3	39	
	Result No.	1	7	٣	4	C)	9	7	00	ወ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	

hemocyanin chain b	probable MYB trans	hypothetical prote	TonB-dependent rec	probable polyketid	endoglucanase homo	alpha-hemolysin BH	hypothetical prote	14K beta-galactosi	hydrolase [importe	sucrose-phosphatas	hypothetical prote	probable regulator	cellulase - Fibrob	glycyl-tRNA synthe	arginine-tRNA liga
внгов	A71448	C72521	D87596	G86925	AB1079	E84003	E84087	LNCH14	AF2657	C97439	T30624	AB0134	857526	D82884	A81323
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657	745	880	1073	2103	800	75	123	135	248	248	255	362	388	473	530
45.3	45.3	45.3	45.3	45.3	44.8	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2
39	9	ტ ტ	3	ტ ტ	38.5	38	38	38	38	38	38	38	38	33	38
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 B40901
equine arteritis virus 1b protein homolog - lactic dehydrogenase virus (isolate LDV-P) (f
Cipercia 30-Sep-1933 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
R;Kuo, L.; Harty, J.T.; Erickson, L.; Palmer, G.A.; Plagemann, P.G.W. J. Virol. 65, 5118-5123, 1991
A; Title: A nested set of eight RNAs is formed in macrophages infected with lactate dehyda A: Reference number: A40901: MUID: 91333066: PMID: 1870216
A; Accession: B40901
A. Status: preliminary
A; Worlecture Type: Inkva A; Residues: 1-540 < XUO>
A;Cross-references: UNIPROT:Q83024; GB:S50064; NID:g233624; PIDN:AAB19478.1; PID:g233625
 C;Superfamily: equine arteritis virus RNA-directed RNA polymerase
Query Match 57.0%; Score 49; DB 2; Length 540;
Hest Local Similarity 75.0%; Fred. No. 2.7; Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 RHWGLQENTREG 14
Db 50 RHRGVLFNTRFG 61

Conserved hypothetical protein SPBC30B4.08 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40174
R;Lyne, M.; Rajandaream M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
A;Reference number: Z21909
A;Reference number: Z21909
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-277 < LyNN
A;Residues: 1-277 < Ly

Gaps .. 0 Query Match 51.2%; Score 44; DB 2; Length 277; Best Local Similarity 87.5%; Pred. No. 8.9; Matches 7; Conservative 0; Mismatches 1; Indels

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2 LRHWGLQF 9

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A; Accession: S57763

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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, c. A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: A64143
A;Actatus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted to the EMBL Data Library, September 1998
A;Reference number: 220257
A;Accession: T26721
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1.128 AMID.
A;Cross-references: UNIRPOT:09XX30; EMBL:AL031633; PIDN:CAA21010.1; GSPDB:GN00021; CESP:)
A;Experimental source: clone Y39AlA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription regulator mmsR - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Jate: 0.4 Mar. 1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42902; S27601
R;Steele, M.I.; Lorenz, D.; Hatter, K.; Park, A.; Sokatch, J.R.
A;Steele, M.I.; Lorenz, D.; Hatter, K.; Park, A.; Sokatch, J.R.
A;Title: Chem. 257, 13588-1359, 1992
A;Title: Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO encoding meth
A;Reference number: A42902; MUID:92317087; PMID:1339433
                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P71339; GB:U32696; GB:L42023; NID:g1573057; PIDN:AAC21791.1; A;Note: best homolog was a hypothetical protein (insertion element IS1223) from Lactobaci
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A;Experimental source: PAO, ATCC 15692
A;Note: sequence extracted from NCBI backbone (NCBIN:107704, NCBIP:107706)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Y39AlA.20 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26721
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50.0%; Score 43; DB 2; Length 128;
Best Local Similarity 72.7%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 3; Indels
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C;Superfamily: hypothetical protein b2382
C;Keywords: DNA binding; transcription regulation
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A;Map position: 3
A;Introns: 33/2; 47/1; 77/3; 107/1
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Best Local Similarity 80.0
Matches 8; Conservative
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A, Status: preliminary
A, Molecule type: DNA
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R; Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Laubber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Msauda, S.; Maucell
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
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T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasta, K.; Yoshida, K.; Altitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Accession: A; Roches, B.; MulD:9384377
A; Accession: A; Alobso, MulD:98044033; PMID:9384377
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A;Molecule type: DNA
A;Rosidues: 1-363 <GLA>
A;Rosidues: 1-363 <GLA>
A;Cross-references: UNIPROT:P39576; EMBL:Z49992; NID:g895746; FIDN:CAA90289.1; PID:g8957
A;Cross-references: UNIPROT:P39576; EMBL:Z49992; NID:g895746; FIDN:CAA90289.1; PID:g8957
B;Glassr, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu,
A.; Rapoport, G.; Danchin, A.
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A;Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fx
A;Reference number: S39655; MUID:95020537; PMID:7934828
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A;Experimental source: strain 168
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                                                                                                                                                                                                       branched-chain amino acid aminotransferase homolog ywaA - Bacillus subtilis C; Species: Bacillus subtilis C; Species: Bacillus subtilis C; Species: Bacillus subtilis C; Species: Bacillus subtilis C; Sacession: S57763; S39655; Ā70050 R; Glaser, P.; Lubochinsky, B.; Danchin, A. submitted to the RmBL Data Library, July 1995 A; Description: Bacillus subtilis cel operon.

A; Reference number: S57758
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C,Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C,Accession: A64143
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                    LEHWGLOF 223
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A; Residues: 1-363 < KUN>
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R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Reference number: A95842; MUD:21396508; PMID:11481431

A;Reference number: A95842; MUD:21396508; PMID:11481431

A;Recession: D95844

A;Recession: D95844

A;Residues: L-412 < KUR>
A;Rosion: D85845

A;Residues: L-412 < KUR>
A;Rosion: C95845

A;Reperimental source: strain 1021, megaplasmid pSymB

B;Gallbert, F.; Pinan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Rederspiel, N.A.; Fisher, R.F.;

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A;Authors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, Hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weils, D.H.; Wong, K.; Yeh, K.(A)

A;Attle: The composite genome of the legume symbiont sinorhizobium meliloti.

A;Genetics:
A;Geneti
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Pipelvecointo, VG; Kapatara, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The ganome sequence of the facultative intracellular pathogen Brucella melitens; A;Reference number: AD3252; PMID:11756688
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A;Residues: UNIPROT:Q8YFF0; GB:AE008917; PIDN:AAL52753.1; PID:g17983585; GSPDB:G:A;Experimental source: strain 16M
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C;Species: Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
B;Yoshida, K.; Seki, S.; Fujita, Y.
DNA Res. 1, 157-162, 1994
A;Title: Nucleotide sequence and features of the Bacillus licheniformis gnt of A;Reference number: PC2201; MUID:96051988; PMID:8535972
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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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Pred. No. 34;
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Pred. No. 35;
1; Mismatches
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Best Local Similarity 66.7
Matches 8; Conservative
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A;Molecule type: DNA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Pseudomonas aeruginosa
C;Date: 15-89-2000 #text_change 09-Jul-2004
C;Accession: F83198
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: B83198
A;Status: preliminary
A;Residues: 1-307 <STO>
A;Cross-references: UNIPROT:P28809; GB:AE004778; GB:AE004091; NID:g9949722; PIDN:AAG0695
A;Escidues: arrain PA01
C;Genetics:
A;Gene: mmsR; PA3571
C;Superfamily: hypothetical protein b2382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypochetical protein KOIC8.3 - Caenorhabditis elegans
C;Date: Caenorhabditis elegans
C;Date: Caenorhabditis elegans
C;Date: Scacession: T23175
R;Sins, M.
R;Sins, M.
A;Reference number: Z19702
A;Accession: T23175
A;Accession: T
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                                                                                                                                                                                                                                                                                                                                                                                       transcription regulator MmsR PA3571 [imported] - Pseudomonas aeruginosa (strain PAO1)
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Pred. No. 45;
2; Mismatches 3; Indels
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A,Map position: 2
A,Introns: 31/1; 74/1; 181/3; 392/2; 416/1; 489/3; 551/1
P;78-546/Domain: animal histidine decarboxylase homology <HDC>
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Similarity 54.5%;
6; Conservative
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                                                                                                                                                               144 LRHWGLQ 150
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Best Local Similarity
Matches 6; Conserv
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Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative '
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Best Local Similarity 46.2%;
Matches 6; Conservative
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231 LRHWGVTFIGNF
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                                     A, Residues: 1-147 <YOS>
A, Cross-references: UNIPROT:Q45292, DDBJ:D31631; NID:g563948; PIDN:BAA06500.1; PID:g5639
C;Gene: Cs.
A, Gene: cug
C;Superfamily: Bacillus licheniformis oug protein
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Cipace: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Unl-2004
Cipace: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Unl-2004
Cipace: 05-Unl-2004
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidon, J., Hockey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95140
A;Accession: H9
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A;Modecule type: DNA
A;Residues: 1-265 «XIII»
A;Cross-references: UNIPROT:Q97QJ1; UNIPROT:Q8DPM4; GB:AE007317; PIDN:AAK99900.1; PID:g1
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Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Cipacession: H98008
RHOSkins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F. R.; LeBlanc, D.J.; Lee, L.W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N. Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; Artitle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
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                                                                                                                                                                                                                                                                    Score 41; DB 2; Length 147; Pred. No. 14; 0; Mismatches 2; Indels
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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    A; Molecule type: DNA
A; Residues: 1-147 < YOS>
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C;Species: Yerainia pestis
C;Date: 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 07-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 07-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
R;Pacresion: AP0146
R;Parkhill, 01: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I
I.M.; Ritherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                            C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT:09X204; GB:AE001608; GB:AE000512; NID:g4982233; PIDN:AAD3674:A;Experimental source: strain MSB8 C,Genetics: A,Genetics: A,
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A,Molecule type: DNA
A,Residues: 1-285 <KUR>
A,Residues: 1-285 <KUR>
C,Genetics: WIPROT:Q8ZGT5; GB:AL590842; PIDN:CAC90033.1; PID:g15979255; GSPDB:GN
A,Genetics: A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 399, 323-329, 1999
Affile: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequesterance number: A72200; WUD:99287316; PMID:10360571
A;Accession: B7226
A;Accession: Dr21amary
A;Gratue: prellminary
A;Molecule type: DNA
A;Residues: 1-277 <ARN>
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                                                                Score 41, DB 2; Length 285;
Pred. No. 28;
2; Mismatches 5; Indels
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hypothetical protein - Thermotoga maritima (strain MSBB)
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Pred. No. 28;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: November 10, 2004, 15:55:10 Job time : 5.12456 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 14:50:40; Search time 25.1423 Seconds (without alignments) 343.270 Million cell updates/sec Run on:

US-10-092-750-228 86

1 TLRHWGLQFNTRFGV 15 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched: 1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q6jhz7 homo sapien			Q83018 lactate deh			Q9ulfO leishmania						bacillu	Q6fjn1 candida gla	plasmod						P28809 pseudomonas	Q82pa3 streptomyce		Q7mye6 photorhabdu						σ	Q21087 caenorhabdi
OI	Q6JHZ7	Q83024	Q7SKF3	083018	Q8 Y066	HEMZ PASMU	Q9U1F0	Q8A8V1	Q7URC4	9XEN6O	013668	074367	ILVE BACSU	Q6FJN1	Q7RKW9	Q7PPM7	Y112 HAEIN	Q89TR3	Q9ANL4	ALKE BABBO	MMSR_PSEAE	Q82PA3	Q9L149	Q7MYE6	Q93H27	CINA GLOVI	Q82WN8	Q7V0Y9	Q7MYB5	600880	Q21087
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Score	49	49	4.0	4	47	47	46	45	45	44.5	44	44	44	44	44	44	43	43	43	43	43	43	43	43		43	43	43	42	42	42
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Q95zs2 caenorhabdi Q6kaf3 oryza sativ	Bad19111 oryza sat Q9u5d7 plautia sta 092vb2 rhizobium m	Q8g2g9 brucella su Q8yff0 brucella me	Q45292 bacillus li Q8dpm4 streptococc	Q97qj1 streptococc Q9x204 thermotoga	Q8zgt5 yersinia pe Aas61198 yersinia	P31975 mycobacteri
Q95ZS2 Q6KAF3	BAD19111 Q9U5D7 Q92VR2	Q8G2G9 Q8YFF0	YOUG BACLI O8DPM4	Q97QJ1 Q9X204	Q8ZGT5 AAS61198	ADHC MYCTU
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ALIGNMENTS

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1 TLRHWGLQFNTRFG 14
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150 RHRGVLFNTRFG 161
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Best Local Similarity
Matches 9; Conserv
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Q8Y066;
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A Bharia P., Mandal D., Chakrabarti S.;
Bharia P., Mandal D., Chakrabarti S.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
BMSL; AY309063; AAQ19802.1; -.
BMSL; AY3090621; C.:Integral to membrane; IEA.
GG; GG:0019028; C::Viral envelope; IEA.
GG; GG:0019031; C::Viral envelope; IEA.
GG; GG:0019031; C::Viral envelope; IEA.
RG; GG:0019031; C::Viral envelope; IEA.
RG; GG:0019031; C::Viral envelope; IEA.
RG; GG:0019031; C::Viral envelope; IEA.
RINTERPOS IPR000777; GF120.
R Fam; PRO0515; GF120.
R Pfam; PRO0517; GP120.
R AIDS: Coat protein; Envelope protein; Glycoprotein; Polyprotein;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Polyprotein 1b (Fragment).
Polyprotein 1b (Fragment).
Victuated edhydrogenase-elevating virus (LDV).
Viruses; SSRNA positive-strand viruses, no DNA stage; Nidovirales;
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                                                                                                                                 Query Match 57.0%; Score 49; DB 2; Length 540; Best Local Similarity 75.0%; Pred. No. 11; Matches 9; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.0%; Score 49; DB 2; Length 882; illarity 61.5%; Pred. No. 19; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          882 AA; 101055 MW; 3274398DE6451D82 CRC64;
InterPro; IPR001607; Znf_UBP.
Pfam; PP06332; Corona_RP01; 1.
Pfam; PP02148; zf-UBP; 1.
NON TER 540 A4; 60507 MW; A6IF2A424FFB974E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus 2.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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50 RHRGVLFNTRFG 61
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EXPLINE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=Plagemann P.G.;

A Faberg K.S., Plagemann P.G.;

The envelope proteins of lactate dehydrogenase-elevating virus and their membrane topography.";

RI JU1546; AAA88664.1;

REBL; U15146; AAA88664.1;

BRBL; U15146; AA88664.1;

CO 00003723; F.RNA binding; IEA.

GO; GO:0003723; F.RNA binding; IEA.

GO; GO:0003724; F.RNA binding; IEA.

RO; GO:0003768; F.RNA-directed RNA polymerase activity; IEA.

BR GO; GO:0003968; F.RNA-directed RNA polymerase activity; IEA.

BR GO; GO:0003968; F.RNA-directed RNA polymerase activity; IEA.

BR InterPro; IPR007099; RNA_pol_DS PS.

InterPro; IPR007099; RNA_pol_DS PS.

InterPro; IPR007099; RNA_pol_DS-ir.

BR InterPro; IPR001609; ZME UBP.

BR FEAM; PF00443; Viral helicasel.

BR Pfam; PF01443; Viral helicasel; 1.

BR Pfam; PF01448; zf-UBF; 1.
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T. "Genome sequence of the plant pathogen Ralstonia solanacearum.";

T. "Ature 415:497-502(2002)

T. BMB1, AL646063; CAD14880.1;

T. BMB1, AL646063; CAD14880.1;

T. GO, GO.0003824; F:catalytic activity; IEA.

GO, GO.0045735; F:nutrient reservoir activity; IEA.

InterPro, IPR002641; Patatin.

R. Pfani, PF0174; Patatin; 1.

T. Complete proteome; Lipoporcein; Transmembrane.

Complete proteome; Lipoporcein; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Values (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2003 (TrEMBLrel. 20, Last sequence update) 01-MAR-2004 (TEMBLrel. 26, Last amnotation update) PROBABLE LIPOPROTEIN TRANSMENBRANE.

Name-RS04543; OrderedLocusNames-RSc1178; Ralstonia solanacearum (Pseudomonas solanacearum) (Pseudomonas solanacearum).

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.0%; Score 49; DB 2; 75.0%; Pred. No. 31; tive 1; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
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R HSSP; 096496; 1854.

R HSSP; 096496; 1854.

R GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016616; F:oxidoreductase activity; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0006564; P:L-serine biosynthesis; IEA.

R InterPro; IPR002183; ADH zinc.

R InterPro; IPR001945; CytC heme BS.

InterPro; IPR0100345; CytC heme BS.

R ROSITE; PS001059; ADH Zinc, 1.

R ROSITE; PS00109; CytCCHROWE C; UNKNOWN 1.

R ROSITE; PS00109; CytCCHROWE C; UNKNOWN 1.

R ROSITE; PS00109; CytCCHROWE C; UNKNOWN 1.

R ROSITE; PS001055; D 2 LHYDROXYACID DH 1; 1.

R REAL-Dinding; Oxidoreductase; Zinc.

R RELabinding; Oxidoreductase; Zinc.

R REQUENCE 352 AA; 38370 MW; EF236A475960DE9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Friedlin;
Bothe G., Pohl I., Ivens A.C., Lawson D., Quail M., Rajandream M.A.,
Barrell B.G.;
                                                                                               MEDINE-88146415; PubMed-9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
"A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- CORACTOR: Zinc (By similarity).
EMBL; AL121862; CABS8398.1; --
HSSP; O96496; 1E3J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LRHWGLQFNTRF 13
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Q8A8V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A COUNTY OF THE SECTION OF THE SECTI
    SO WE WERE THE SERVICE SERVICE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
NADP-dependent alcohol hydrogenase.
Name=1.1063.09;
Leishmania major.
Bikaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TAXID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 41 Last annotation update)
Ferrochelatase (EC 4.99.1.1) (Protoheme ferro-lyase) (Heme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 195 Iron (By similarity).
276 276 Iron (By similarity).
326 AA; 37421 MW; BAAAEEEAC77DE3D5 CRC64;
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InterPro; IRRO1015; Ferrochelatase.
Pfam; PR00162; Ferrochelatase; 1.
ProDom; PD002792; Ferrochelatase; 1.
TIGRFAMS; TIGRS0109; hemb; 1.
PROSITE; PS00534; FERROCHELATASE; 1.
Complete proteome; Heme biosynthesis; Iron; Lyase; Portphrin biosynthesis. Iron (By similarity).
METAL 276 276 Iron (By similarity).
METAL 276 276 Iron (By similarity).
                                                                                                                                                                                                                                                  326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=hemH; OrderedLocusNames=PM0789;
Pasteurella multocida.
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE006117; AAK02873.1; -.
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1 TLRHWGLQFNTRFG 14
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                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetase).
                                                                                                                                                                                                                                                       PASMU
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                                                                                                                                                                Q9U1F0
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Q9U1F0
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STRAIN=VPI-5482 / ATCC 29148;
STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
EMBL; AE016930; AA076173.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 189 AA; 21630 MW; 32FD584DF4482C08 CRC64;
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Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales;
Bacteroidaceae, Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.3%; Score 45; DB 2; Length 189; Best Local Similarity 58.3%; Pred. No. 18; Matches 7; Conservative 2; Mismatches 3; Indels
53.5%; Score 46; DB 2; Length 352; 57.1%; Pred. No. 23; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                       01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
OrderedLocusNames=BT1066;
                                                                                                                                                                                                                                                                                                                                      PRT; 189 AA.
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169 LRYWGVKKGTRVGV 182
                                                                                                                               2 LRHWGLQFNTRFGV 15
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68 LRHWGIQPEVRY 79

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Eukaryota, Metaselegans.
Rhabditidae; Mematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                         Gloeckner F.C., Kube M., Bauer M., Teeling H., Lombardot T., Loudwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                 Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
-!-SINILARITY: Belongs to the heat shock protein 70 family.
BMBL, BX294142; CaD74416.1;
GO, GO:0005524; F:ATP binding; IEA.
InterPror. IPR001023; Hsp70.
PROSITE; PS00297; HSP70.1; 1.
PROSITE; PS00297; HSP70.1; 1.
PROSITE; PS00297; HSP70.2; 1.
ATP-binding; Complete proteome.
SEQUENCE 645 AA; 70160 MM; 2F23DBF17291F2C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 2; Length 645;
Pred. No. 65;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Bristol N2;
Tin-Wollam A., Wohldmann P.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                       01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
10-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Name=chaperone protein DnaK.
Name=chaperone Protein DnaK.
Rhodopirellula baltica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
101-UNAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Y42H9B.2.
ORFNames=Y42H9B.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 2325 AA.
                             PRT;
                                                                                                                                                                                                                             STRAIN=1;
MEDLINE=22735913; PubMed=12835416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    631 RHWKLEFNAR 640
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                         NCBI_TaxID=117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9N3X8;
                           Q7URC4
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Q9N3X8
RESULT 9
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Gaps
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PROSITE; PS50835; IG_LIKE; 5.
Hypothetical protein.
SEQUENCE 2325 AA; 259163 MW; 6F3E76CA3303338E CRC64;
                            to the EMBL/GenBank/DDBJ databases
                                                                          to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              Waterston R., Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                           Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=pi077;
Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomycetas;
Schizosaccharomycetales; Schizosaccharomycetes;
Schizosaccharomyces.
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O13668;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Pi077 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GLQFNTRFGV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.7%; Score 44.5; DB 2
28.9%; Pred. No. 3e+02;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TLRHW-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 28.9°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                     Waterston R.H.;
Submitted (MAR-2000)
                                                                 Waterston R.;
Submitted (MAR-2000)
                                                                                                                Waterston R.;
Submitted (JUN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
STRAIN=972 h-;
SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                             SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                            SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                          SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
                    Waterston R.H
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RESULT 13
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WEDLINE=21848401; PubMed=11859360;

WEDLINE=21848401; PubMed=11859360;

WEDLINE=21848401; PubMed=11859360;

WOOD V., GWilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squros J., Peat N., Hayles J., Basham D., Bowman S., Anderson J., Brown D., Brown S., Chillingworth T., Churcher C., Collins M., Connor R., Cronin A., Davis P., Felewell T., Fraser A., Gonlins M., Connor R., Harris D., Hidligo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckell T., Fraser A., Andes L., Jones M., Leather S., McDonald S., McLean J., McDonay P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA Oliver K., O'Neil S., Sauros R., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Ander S., Anderson J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S., Gabel C., Fuchs M., Duserhoft A., Erizcc C., Holzer B., Moetlin S., Andels M., Schafer M., Schafer M., Moltier S., Galber C., Fuchs M., Dusens S., Lelaure V., Moetler S., Galbert H., Borzym K., Langer I., Beck A., Lehrach H., Wenther S., Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S., Andelber F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S., Bantto J., Moreno S., Armstrong J., Forsburg S.L., Abrahler L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
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              Machida M., Yamazaki S., Kunihiro S., Tanaka T., Kushida N., Jinno K., Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Cguchi A., Nagai Y., Sakai M., Acki K., Ogura K., Kudoh Y., Kikuchi H., Zhang M.Q., Yanagida M., "A 38 kb segment containing the cdc2 gene from the left arm of fission yeast Chromosome II: sequence analysis and characterization of the genomic DNA and cDNAs encoded on the segment.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                          STRAIN-972 h.;

Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

BMBL; AB004539; BAA21459.1; -.

EMBL; AB004539; BAA21459.1; -.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0004527; F:exonuclease activity; IEA.

InterPro; IPR06055; Exonuclease.

ERM, PR00499; EXOINC. X-T; 1.

SMART; SM00499; EXOINC X-T; 1.

SMART; SM00499; EXOINC X-T; 1.
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01-MAR-2004 (TrEMELrel. 26, Last annotation update)
Name-Special veconuclease; no apparent S. cerevisiae ortholog.
Name-Special 08,
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.2%; Score 44; DB 2; Length 231; 87.5%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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MEDLINE=20089027; PubMed=10620777;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 87.5 ses 7; Conservative
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                                                                                                                                                                                                                                                                        FROM N.A.
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RX ENGLINE=98044033; PubMed=9384377; DOI=10.1038/36786;

RA KUNGE F. Ogdaswara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A.M., Barchert S.,

RA Derrises R., Bourseler L., Brans A., Bardmun V., Erignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Captano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusternoff A., Ehrlich S.D., Emmerson P.T.,

RA Fritz C., Fujita M., Fujita Y., Fram S., Galizzi A., Galleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Ghiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,

RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klasut A.,

RA Lazarevic V., Lee S.M., Levine A., Lardinois S., Lauber T.,

RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,

RA Medigue C., Medina N., Mallado R.P., Mizuno M., Mocett D., Nakai S.,

RA Doback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,

RA Prescott A.M., Presecan E., Puic P., Purnelle B., Rapoport G.,

RA Rose M., Sadaie Y., Sato T., Sacnlan E., Schleich S., Schroete R.,

RA Scoffone P., Sekiguchi J., Sacnlan E., Tarkahashi H.,

RA Takemaru K., Takeuchi M., Tamakchi T., Tarkahashi H.,

RA Takemaru K., Takeuchi M., Tamakchi T., Tarkahashi H.,

RA Takemaru K., Takeuchi M., Tamakchi R., Tanaka T., Terpetra P.,

RA Takemaru K., Takeuchi M., Tamakchi R., Tanaka T., Terpetra P.,

RA Takemaru K., Takeuchi M., Wambutt R., Wanden E., Wedler H.,

RA Tagnoni H., Wandel E., Wandel E., Wedler H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1998 (Rel. 36, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
Putative branched-chain-amino-acid aminotransferase (EC 2.6.1.42)
(BCAT) (Vegetative protein 85) (VEG85).
BCAT) (Vegetative protein 85) (VEG85).
Bacillus subtilis.
Bacillus subtilis.
Bacillus subtilis.
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87.5%; Pred. No. 40;
ive 0; Mismatches 1; Indels
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Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 AA; 32282 MW; 79CD4FFCDC954C89 CRC64;
"The genome sequence of Schizosaccharomyces pombe.";
                      Nature 415:971-880(2002).

EMBL, AL031262, CAA20321.1; -
PIR, T40174; T40174.

GeneDB SPOMDe; SPBG130B4.0B; -.
GO; GO:0003674; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004527; F:Exonuclease activity; IEA.
InterPro; IPR006055; Exonuclease.
Fram, PF00929; Exonuc X-T; 1.
SWART; SMO0479; EXOIIT; 1.
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les 7; Conserva
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P39576;
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SEQUENCE
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blackasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Miller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Sandou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
A Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=1236885;
Carlton J.M., Angiuoli S.V., Suh B.B., Kooli T.W., Pertea M.,
Silva J.C., Emolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
Cho J.K., Quackenbush J., Sedgah M., Shoabibi A., Cumings L.M.,
Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
Carucci D.J.;
    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp[Pl1745 Saccharomyces cerevisiae YMR235c RNAl GTPase activating protein.
                                                                                                                         Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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NCBI_TaxID=73239;
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InterPro; IPR001611; LRR.
InterPro; IPR003590; LRR, 4.
PRINTS; PR00109; LEURICHRPT.
SMART; SM00368; LRR. R1; 5.
RROITENCE 402 AA; 45455 MW; 34C30E376A5AA95F CRC64;
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Last annotation update)
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46.7%; Pred. No. 58;
tive 5; Mismatches
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Nature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; CR380959; CAG62539.1; -.
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 46.73
Matches 7; Conservative
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                                                                                                       ORFNames=CAGLOM04961g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aldo-keto reductase.
Name=PY02780;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Q7RKW9
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                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                             "Bacillus subtilis genome project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees.";
Mol. Microbiol. 10:371-384(1993).
Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
                                                                                                                                                                                                           Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W., Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I., Presecan E., Santana M., Schneider E., Schweizer J., Vertes A., Rapoport G.,
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ProDom; PD01961; Aminotran 4; 1.
TIGRPAMs; TIGR01123; ilvE IT; 1.
PROSITE; PS00770; Am TRANSFE CLASS 4; 1.
Aminotransferaes, Branched-chain amino acid biosynthesis;
Complete proteome; Direct protein sequencing; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 0
196 196 Pyridoxal phosphate (By similarity)
362 AA; 40191 MW; FFBA681A5FDC7057 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, 015382; 1KT8.
Subtilist; BG10546; ywaA.
InterPro; IPR001544; Aminotrans IV.
InterPro; IPR005786; B aminotransII.
                                                                                                                                                                   STRAIN=168;
MEDLINE=95020537; PubMed=7934828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, Z49992; CAA90289.1; -. EMBL, 299123; CAB15881.1; -. EMBL, X73124; CAA51556.1; -. PIR; S57763; SS7763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.00,
A Conservative
                                                                                                                                                 SEQUENCE OF 1-57 FROM N.A.
                                                                                                          Nature 390:249-256(1997),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 LKHWGLQVSER 278
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BINDING
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402 AA.

PRELIMINARY;

QGFJN1 QGFJN1;

RESULT 14 Q6FJN1 ID Q6 AC Q6

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Gaps

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Length 402; Indels

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0; Gaps
                                                                Query Match 51.2%; Score 44; DB 2; Length 779; Best Local Similarity 57.1%; Pred. No. 1.2e+02; Matches 8; Conservative 1; Mismatches 5; Indels
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Search completed: November 10, 2004, 15:53:45 Job time : 27.2193 secs

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November 10, 2004, 11:41:17; Search time 8.04167 Seconds (without alignments) 222.664 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                US-10-092-750-22
140
1 ARGDFAQAAQCIWLALRALGRPLPTSH 27
                                                                                                                                                                                                                                                                                                                                        478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                  Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
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                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 38, Appl Sequence 38, Appl Sequence 6, Appl Sequence 54, Appl Sequence 54, Appl Sequence 25034, A Sequence 25034, A Sequence 233, Appl Sequence 2, Appl Sequence 24639, A Sequence 4639, A Sequence 24639, A
SUMMARIES	US-08-131.365B-38 US-08-668-123-38 US-08-668-123-38 US-09-526-257-60 US-09-522-666-6 US-09-252-991A-17953 US-09-252-991A-17953 US-09-252-991A-17953 US-09-252-991A-17953 US-09-252-991A-17953 US-09-252-991A-17953 US-09-252-991A-17953 US-09-252-991A-17953 US-08-46-390-2 US-08-46-390-2 US-08-46-390-2 US-08-46-390-2 US-08-46-390-2 US-08-46-390-2 US-08-483-651-2 US-08-483-651-2 US-08-483-61-2 US-08-483-61-2 US-08-483-61-2 US-08-483-61-2 US-08-483-61-2 US-08-483-61-2 US-09-252-991A-1295 US-09-252-991A-1295 US-09-252-991A-1295 US-09-252-991A-1295 US-09-252-991A-1295 US-09-252-991A-1295 US-09-252-991A-1295
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Length	11111111111111111111111111111111111111
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Score	1000 1000 1000 1000 1000 1000 1000 100
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.. 0

Gaps

.. 0

Length 1147; Indels 0

Query Match
100.0%; Score 140; DB 1;
Best Local Similarity 100.0%; Pred. No. 4.2e-12;
Matches 27; Conservative 0; Mismatches 0;

LENGTH: 1147 animo acids
ryPE: amino acid
TOPOLGOT: linear
MOLECULE TYPE: protein
US-08-131-3658-38

1 ARGDFAQAAQQLWLALRALGRPLPTSH 27

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Sequence 18711, A Sequence 18711, A Sequence 18711, A Sequence 16863, A Sequence 16983, A Sequence 2, Appli Sequence 4, Appli Sequence 20, Appli Sequence 5, Appli		TING BINDING
US-09-252-991A-25512 US-09-252-991A-18711 US-09-252-991A-18711 US-09-252-991A-16863 US-09-252-991A-16863 US-09-485-6328-2 US-09-485-6328-2 US-09-229-591A-2922 US-09-229-591A-4 US-09-632-291A-4 US-09-632-291A-4 US-09-252-991A-18082 US-09-356-991A-18082 US-09-356-991A-18082 US-09-356-991A-18082 US-09-256-991A-18082 US-09-268-480-5 US-09-568-480-5 US-09-568-480-5	ALIGNMENTS	COMPOSITIONS RELA EGULATORY ELEMENT rkee , 355B , 355B
32.1 605 4 31.8 198 4 31.8 198 4 31.4 198 4 31.4 221 4 31.4 7257 3 31.4 7257 3 31.4 7257 3		SULT 1 Sequence 38, Application US/0813136 Sequence 38, Application US/0813136 Sequence 38, Application US/0813136 Sequence 38, Application US/0813136 Sequence 38, Application Michael S. APPLICANT: Brown, Michael R. APPLICANT: Goldstein, Joseph L. TITLE OF INVENTION: METHODS AND TITLE OF INVENTION: METHODS AND TITLE OF INVENTION: PROTEINS NUMBER OF SEQUENCES: 64 COUNTRY: U.S.A. STREET: P.O. Box 4433 CITY: Houston STREET: PLOYON GISK COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: OF COMPONION: POPERATING SYSTEM: PC-DOS/NS-D SOFTWARE: Patentin Release #1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/131 FILING DATE: O1-OCT-1933 CLASSIFICATION NUMBER: 32,165 REFERENCE/DOCKET NUMBER: USD TELEPHONE: (512) 414-757 INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS: LENGTH: HADAR. TOPPY. ACID ACID ACID ACID ACID ACID ACID ACID
2000 3300 3300 3300 3300 4444 4444 4444	8	NESULT 1 US-08-131-3658-38 Sequence 38, Appl. Sequence 38, Appl. Sequence 38, Appl. APPLICANT: B. COMPRESSED: COMPRESSED: COMPRESSED: COMPUTER READING S. SOPTARE: D. COMPUTER READING S. COMPUTER READING S. COMPUTER: APPLICATION REFINING DATE CLASSIFICATION REGISTANTING S. SECIENCE DATE CLASSIFICATION REGISTANTING S. CLASSIFICATION REFERENCE DATE TELEBRANCE DATE TELEBRANCE DATE TELEBRANCE CHARL TELEBRANCE CHARL TELEBRANCE CHARL TELEBRANCE CHARL TOWNER THE SERVICE THE SE
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STREET: P.O. BCCITY: Houston STATE: Texas COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Human
US-09-360-237-60
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LENGTH: 1049
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Betent No. 6222962

GENERAL INFORMATION

APPLICANT: BROWN, MICHAEL S.

APPLICANT: GENERAL S.

APPLICANT: GENERAL S.

APPLICANT: AMSON, ROBER B.

APPLICANT: RAWSON, ROBER B.

APPLICANT: SAKAI, JURO

TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF

FILE REPERENCE: UTXD:567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                            Local Similarity 100.0%; Score 140; DB 2; Length 1147; Best Local Similarity 100.0%; Pred. No. 4.2e-12; Matches 27; Conservative 0; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: A.C. COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 14-UW-1996
CLASSIFICATION NUMBER: US/08/669,123
FILING DATE: 14-UW-1996
FILING DATE: 10-CCT-1993
FILING DATE: 01-CCT-1993
ATPORNEY/AGENT INFORMATION:
NAMM: PARKEY, DAVIG L.
RECISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 32,165
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TO NOT THE TELECOMMUNICATION INFORMATION:
TO NOT THE TELECOMMUNICATION INFORMATION:
TO NOT THE TELECOMMUNICATION INFORMATION INFORMATION:
TO NOT THE TELECOMMUNICATION INFORMATION INFORMATIO
594 ARGDFAQAAQQLWLALRALGRPLPTSH 620
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MOLECULE TYPE: protein

US-08-668-123-38
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Score 75; DB 2; Length 1141; Pred. No. 0.014;
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                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              586 ARGDFAAAANLQTCLAVLGRALPTS 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Pseudomonas aeruginosa
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 65.4%;
Matches 17; Conservative
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TELEFAX: (512) 474-7577 INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1141
                                                                                        TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-668-123-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-18345
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US-09-252-991A-25034
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; Sequence 54, Application US/08668123
; Patent No. 5891631
; GENERAL INFORMATION:
    APPLICANT: Briggs, Michael S.
    APPLICANT: Briggs, Michael R.
    APPLICANT: Goldstein, Joseph L.
    TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
    TITLE OF INVENTION: PROTEINS
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold, White & Durkee
    STREET: P.O. Box 4433
; CITE OF INVENTION: PROTEINS
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold, White & Durkee
    STREET: P.O. Box 4433
; CITE OF INVENTION: PROTEINS
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER IBM PC Compatible
COMPUTER: Ploppy disk
COMPUTER: Plan PC Compatible
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,123
FILING DATE: 14-UN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/131,365
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: PARKET, David L.
REGISTRATION NUMBER: 32,165
REGISTRATION NUMBER: 32,165
REGISTRATION NUMBER: UTSD:372/PAR
TELECOMMULICATION INFORMATION:
TELEDHONE: (512) 418-3000
                                                                                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

AIGNATION:

ATTORNEY/AGENT INPOMMATION:

NAME:

REGISTRATION NUMBER:

ATTORNEY/AGENT INPOMMATION:

NAME:

REGISTRATION NUMBER:

ATTORNEY/AGENT INPOMMATION:

NAME:

REGISTRATION NUMBER:

TELEPHONE:

TELEPHONE:

(512) 414-7577

INPORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 75; DB 1;
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.6%; Score 75; DB Best Local Similarity 65.4%; Pred. No. 0.01 Matches 17; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ARGDFAQAAQQLWLALRALGRPLPTS 26
                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Texas
COUNTRY: U.S.A.
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-131-365B-54
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US-08-668-123-54
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Sequence 18345, Application US/09252991A; Sequence Tolor Sequen
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US-09-252-991A-25034

US-09-252-991A-25034

Sequence 25034, Application US/09252991A

Sequence 25034, Application US/09252991A

Sequence 25034, Application US/09252991A

Sequence 25034, Application US/09252991A

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25034

LENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 48.0%; Pred. No. 45;
Matches 12; Conservative 4; Mismatches 6; Indels
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1777 DIEOGKLOMWYDLFPKALGRPGP 1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-252-991A-31885
; Sequence 31885, Application US/09252991A
; Patent No. 6551798;
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 DFAQAAQQLWLAL - RALGRPLP 24
                 US-09-382-552-2

; Sequence 2, Application US/09382552

; Patent No. 667309

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AAQQLWLALRALGRPLPTSH 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-382-552-2
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                                                                                                                                                                                                              Sequence 17953, Application US/09252991A

Batent NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PRODOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17953
LENGTH: 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 233, Application US/09382552

Sequence 233, Application US/09382552

Sequence 233, Application US/09382552

GENERAL INFORMATION:

APPLICANT: Liu, Jing
APPLICANT: Ho, Magasshi

APPLICANT: Matsuda-Asada, Chie

APPLICANT: Matsuda-Asada, Chie

TITLE OF INVENTION: DYSFRELIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB

TITLE OF INVENTION: GIRDLE MUSCULAR DYSTROPHY

FILE REFERENCE: 00786/399002

CURRENT APPLICATION NUMBER: US/09/382,552

CURRENT APPLICATION NUMBER: US/09/382,552

CURRENT FILING DATE: 1999-08-25

EARLIER FILING DATE: 1998-08-25
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34.3%; Score 48; DB 4; Length 988;
Best Local Similarity 47.8%; Pred. No. 1.1e+02;
Matches 11; Conservative 3; Mismatches 7; Indels
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                        Indels
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                        12;
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Best Local Similarity 36.0%; Pred. No. 51; Matches 9; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.3%; Score 48; DB Best Local Similarity 46.7%; Pred. No. 96; Matches 14; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 233
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 233
LENGTH: 988
                                                                                                1 ARGDFAQAAQQLWLALRALGRPLPT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Homo sapiens
US-09-382-552-233
                                                                                                                                                                                                         JS-09-252-991A-17953
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US-09-382-552-233
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE POF 10196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31865
APPLICANT: Brown, Jr., Robert H.
APPLICANT: Liu, Jing
APPLICANT: Liu, Jing
APPLICANT: Liu, Jing
APPLICANT: Liu, Jing
APPLICANT: Ho, Mesachi
APPLICANT: Ho, Mesachi
APPLICANT: Ho, Mesachi
APPLICANT: Ho, Mesachi
APPLICANT: Matsuda-Asada, Chie
APPLICANT: Matsuda-Asada, Chie
APPLICANT: Matsuda-Asada, Chie
APPLICANT: Matsuda-Asada, Chie
APPLICANTION: DSFERLIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB
TITLE OF INVENTION: GIRDLE MUSCULAR DYSTROPHY
FILE REFERENCE: 0796/399002
CURRENT APPLICATION WUMBER: US/09/382,552
CURRENT APPLICATION NUMBER: US/09/382,552
CURRENT FILING DATE: 1999-08-25
BARLIER APPLICATION NUMBER: US 60/097,927
BARLIER FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 233
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 5686562
GENERAL INFORMATION:
APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.6%; Score 47; DB 4; Length 501; Best Local Similarity 50.0%; Pred. No. 75; Matches 10; Conservative 3; Mismatches 7; Indels
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Best Local.Similarity 47.8%; Pred. No. 2.6e+02;
Matches 11; Conservative 3; Mismatches 7;
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| Sequence 2, Application US/08467781
| Sequence 2, Application US/08467781
| Patent No. 5780596
| GENERAL INFORMATION |
| APPLICANT INFORMATION |
| TITLE OF INVENTION | NOVEL MALIGNANT CELL TYPE MARKERS OF THE
| TITLE OF INVENTION | NOVEL MALIGNANT CELL TYPE MARKERS OF THE
| TITLE OF INVENTION | NOVEL MALIGNANT CELL TYPE MARKERS OF THE
| TITLE OF INVENTION | NOVEL MALIGNANT CELL TYPE MARKERS OF THE
| TITLE OF INVENTION | NOVEL MALIGNANT CELL TYPE MARKERS OF THE
| TITLE OF INVENTION | NOVEL MALIGNANT CELL TYPE MARKERS OF THE
| STREET | 125 HIGH STREET | THERET | STREET | 125 HIGH STREET |
| CITY: BOSTON | STREET | MA | COUNTRY: USA | COUNTRY: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 1; Length 639;
Pred. No. 98;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 1; Length 639;
Pred. No. 98;
4; Mismatches 7; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PER PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RILING DATE:
FILING DATE:
CLASSIPICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: November 10, 2004, 12:32:33 Job time : 9.04167 secs
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION: MAME: PITCHER ESQ. EDGUND R
REGISTRATION NUMBER: 27.829
REFERENCE/DOCKET NUMBER: MIP-013
TELECOMMUNICATION INFORMATION:
TELEPAK: (617) 248-7000
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: | |||||:: ||
444 ARKAHQLWLSVEALKYSMKTS 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.6%;
Best Local Similarity 47.6%;
Matches 10; Conservative
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Best Local Similarity 47.6%;
Matches 10; Conservative
                                     INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                  : 639 amino acids
amino acid
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amino acid
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                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-08-470-950-2
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| Patent No. 5698439
| GENERAL INFORMATION
| APPLICANT: INFORMATION: GARY
| APPLICANT: INDGARD, GRAHAM P
| TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
| TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
| NUMBER OF SEQUENCES: 6
| CORRESPONDENCE ADDRESS: ADDRESSE: TESTA, HURWITZ & THIBEAULT STREET: 125 HIGH STREET
| CITY: BOOTON
| STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
33.6%; Score 47; DB 1; Length 639;
Best Local Similarity 47.6%; Pred. No. 98;
Matches 10; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                              CITY: BOSTON

STATE: MA

CONTRY: USA

ZIP: US110

COMPUTER READABLE FORM:

MEDIUM TYPE: FIDAPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,390

FILING DATE: 06-UN-1995

CLASSIFICATION: 435

ATTORNEY AGENT INFORMATION:

NAME: PITCHER ESO, EDWUND R

REGISTRATION NUMBER: WIPP-013

TELECOMMUNICATION INFORMATION:

TELECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIDY TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,950
FILING DATE: 06-JUN-1995
CLASSIFICATION: S3 6
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 ARKAHOLWLSVEALKYSMKTS 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 639 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-466-390-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-470-950-2
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us-10-092-750-22.rapb

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November 10, 2004, 15:53:52; Search time 26.0417 Seconds (without alignments) 366.225 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/PCT_PEW PUBLOBD:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_PEW PUBLOBD:*

3: /cgn2_6/ptodata/1/pubpaa/DSO_NEW PUBLOBD:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/USO0NBW.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Title: US-10-092-750-22
Perfect score: 140
Sequence: 1 ARGDFAQAAQQLWLALRALGRPLPTSH 27
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                           Run on:
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No. Score Match Length DB ID

No. Score Match Length DB ID

2 140 100.0 766 15 US-10-108-260A-3088 Sequence 22, Appl 2 140 100.0 1198 15 US-10-108-260A-3088 Sequence 6, Appli 3 140 100.0 1198 15 US-10-429-160-6 Sequence 6, Appli 6 74 52.9 1141 16 US-10-741-601-57 Sequence 557, Appli 6 74 52.9 1141 16 US-10-741-601-57 Sequence 558, Appli 9 54.5 38.9 468 11 US-09-388-26-28054 Sequence 2260, Appli 9 54.5 38.9 551 9 US-09-768-826-40 Sequence 2260, Appli 1 54.5 38.9 555 9 US-09-33-245-2260 Sequence 58, Appli 1 54.5 38.9 565 14 US-10-093-463-138 Sequence 190, Appli 1 54.5 38.9 565 14 US-10-093-463-138 Sequence 190, Appli 1 54.5 38.9 565 14 US-10-093-463-138

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ce 192, App	356053,	174932,	108154,	41739, A	104413,	366972,	39114, A	313297,	54215, A	49178, A	313295,	1187, Ap	307480,	138612,	167918,	4059, Ap	119278,	43433, A	70151, A	250826,	150984,	53833, A	214213,	258037,	69, Appl	150210,	54, Appl	11915, A	66476, A	2, Appli	411, App
Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	equen	Sequence	equen	Sequence	Sequence	ednen	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence
1-093-463-	1-425-115-	1-437-963	US-10-437-963-108154	US-10-425-114-41739	US-10-437-963-104413	US-10-425-115-366972	US-10-425-114-39114	US-10-425-115-313297	US-10-425-114-54215	US-10-425-114-49178	US-10-425-115-313295	US-09-833-245-1187	US-10-425-115-307480	US-10-437-963-138612	US-10-437-963-167918	US-10-369-493-4059	US-10-437-963-119278	US-10-282-122A-43433	US-10-282-122A-70151	US-10-425-115-250826	US-10-437-963-150984	-425-114-5	-425-115-2	1-424-599-2	-314-657-6	US-10-424-599-150210	1-354-437-	815-242	-282-12	-382-86	÷.
14	17	16	16	15	16	17	15	17	15	15	17	11	17	16	16	14	16	15	15	17	16	15	17	15	14	15	15	σ	15	10	16
778	78	385	884	158	172	177	212	212	334	385	431	119	61	134	181	1095	103	476	1389	111	177	234	249	299	322	330	540	712	712	2080	2080
38.9	36.4	36.1	36.1	35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.4	35.0	35.0	35.0	35.0	34.6	34.6	34.6	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3
54.5	51		50.5	20	20	20	20			20	20	49.5	4	49	49	4	48.5	48.5	48.5	48	48	48	48	48	48	48		48	48	48	48
14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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US-10-092-750-22

US-10-092-750-22

Sequence 22, Application US/10092750

Publication No. US20030032157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Alpin, Julia

TITLE OF INVENTION: Polypeptides Interactive with BCL-XI

FILE REFERENCE: 50036/05002

CURRENT FILING DATE: 2002-03-07

PRIOR RILING DATE: 2001-03-07

PRIOR RILING DATE: 2001-03-07

PRIOR RILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22

IENGTH: 27

TYPE: PRT

CORGATHSM: Homo sapiens

GUELY MARCh MATCH 100.0%; Score 140; DB 14; Length 27;

Best Local Similarity 100.0%; Pred. No. 1.1e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps
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Db 1 ARGDFAQAAQQiwLALRALGRPLPTSH
RESULT 2
US-10-108-260A-3088
; Sequence 3088, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:

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Gaps

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Indels

Length 1198;

Fri Nov 12 14:55:03 2004

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; TYPE: PRT
; ORGANISM: Homo sapiens
; PEATURE:
; OTHER INFORMATION: Clone ID: LIB4750-126-A8_FLI.pep
US-10-425-114-72712
                                                                                                                                                                                                                                            Query Match 100.0%; Score 140; DB 15; Best Local Similarity 100.0%; Pred. No. 4.6e-11; Matches 27; Conservative 0; Mismatches 0;
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) ORGANISM: Homo sapiens
US-10-741-601-558
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US-10-029-386-28054
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US-10-741-601-558
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US-10-741-601-557
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| Sequence 72712, Application US/10425114
| Publication No. US2004003488A1
| GENERAL INFORMATION:
| APPLICANT: Liu, Jingdong
| APPLICANT: Zhou, Yihua
| APPLICANT: Zoven E. |
| APPLICANT: Goveren, Steven E. |
| APPLICANT: Cao, Yongwei E. |
| APPLICANT: Tabaska, Jack E. |
| APPLICANT: Tabaska, Jack E. |
| APPLICANT: Tabaska, Jack E. |
| APPLICANT: APPLICANT: ANGLE: ANGL: ANGLE: ANGLE: ANGLE: ANGLE: ANGLE: ANGLE: ANGLE: ANGLE: ANGL: ANGLE: ANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10429160

Publication No. US20040023276A1

GENERAL INPORMATION:

APPLICANT: Ward, Teresa R

APPLICANT: Linsley, Peter S

APPLICANT: Linsley, Peter S

APPLICANT: Lund, Lund

TITLE OF INVENTION: LXR Ligand Induced Genes and Proteins
FILE REFERENCE: RS0200

CURRENT APPLICATION NUMBER: US/10/429,160

CURRENT FILING DATE: 2003-05-02

PRIOR FILING DATE: 2003-05-03

NUMBER OF SEQ ID NOS: 111

SEQ ID NOS: 111

SEQ ID NO 6

SEQ ID NO 6
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REPERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT APPLING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SECTWARE: Patentin Ver. 2.1
SEQ ID NO 3088
LENGTH: 766
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100.0%; Score 140; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 27; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                     CRGANISM: Homo sapiens US-10-108-260A-3088
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TYPE: PRT
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Publication No. US20040166519A1

GENERAL INFORMATION:
TITLE OF INVENTION: GENERAL SERVICATION AND USES THEREOF

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: GENERAL STENOSIS, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION WHORER: US/10/741,601

CURRENT FILING DATE: 2009-12-22

NUMBER OF SEQ ID NOS: 26415

SEQ ID NO 557

LENGTH: 1141

TYPE: PRT

CREANISM: Homo sapiens

US-10-741-601-557
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Publication No. US20040166519A1

GENERAL INFORMATION:
TITLE OF INVENTION: GENERAL COLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001500

CURRENT PILLING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFITARE: FastSEQ for Windows Version 4.0

LENGTH: 1141
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52.9%; Score 74; DB 16; Length 1141;
Best Local Similarity 65.4%; Pred. No. 0.11;
Matches 17; Conservative 0; Mismatches 9; Indels
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                            645 ARGDFAQALWLALRALGRPLFTSH 671
1 ARGDFAQAAQQLWLALRALGRPLPTSH 27
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; Sequence 8, Application US/09897214
; Patent No. US20020076779A1
; GENERAL INFORMATION:
    APPLICANT: Thayer, Edward C.
    APPLICANT: Thayer, Edward C.
    APPLICANT: Presnell Scott R.
    TITLE OF INVENTION: Loucine-Rich Repeat Proteins, Zlrr7,
    TITLE OF INVENTION: Loucine-Rich Repeat Proteins, Zlrr7,
    TITLE OF INVENTION: Loucine-Rich Repeat Proteins, Zlrr7,
    TITLE OF INVENTION: Zlrr8, and Zlrr9
    TITLE OF INVENTION: 21rr8, and Zlrr9
    CURRENT PELLORION NUMBER: US/09/897,214
    CURRENT FILING DATE: 2001-07-02
    PRIOR PELLING DATE: 2001-07-02
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PastSEQ for Windows Version 3.0
; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
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; Sequence 58, Application US/09768826
; Sequence 58, Application US/09768826
; Patent No. US2002012966A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: 18 human secreted proteins
; TILE REFERENCE: PF512P1
; CURRENT APPLICATION NUMBER: US/09/768,826
; PRIOR APPLICATION NUMBER: PCT/US00/22350
; PRIOR APPLICATION NUMBER: PCT/US00/22350
; PRIOR APPLICATION NUMBER: 60/148,759
        APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR PELICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SEQ ID NO 2260
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Pred. No. 26;
3; Mismatches
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Pred. No. 31;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.9%;
Best Local Similarity 37.5%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 37.5%;
Matches 15; Conservative
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CRGANISM: Homo sapiens
US-09-897-214-8
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US-09-833-245-2260
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US-09-897-214-8
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Sequence 28054, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, DAVID R.
APPLICANT: NUMBER: US/10/029,386
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 28054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
46.4%; Score 65; DB 14; Length 92;
Best Local Similarity 62.5%; Pred. No. 0.17;
Matches 15; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO CHR22_22.0

OTHER INFORMATION: EXPRESED IN HELA, SIGNAL = 4.6

OTHER INFORMATION: EXPRESED IN HELA, SIGNAL = 2.7

OTHER INFORMATION: EXPRESED IN BONE MARROW, SIGNAL = 2.5

OTHER INFORMATION: EXPRESED IN BRAIN, SIGNAL = 3.7

OTHER INFORMATION: EXPRESED IN HEART, SIGNAL = 2.6

OTHER INFORMATION: EXPRESED IN PLACENTA, SIGNAL = 2.6

OTHER INFORMATION: SYPRESED IN PLACENTA, SIGNAL = 2.6

US-10-029-386-28054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40, Application US/09768826

Patent No. US2002001296611

GENERAL INFORMATION:
APPLICANT: Shi et al.
TITLE OF INVENTION: 18 human secreted proteins
FILE REFERENCE: PF512P1

CURRENT APPLICATION NUMBER: US/09/768,826

CURRENT APPLICATION NUMBER: PCT/US00/22350

PRIOR APPLICATION NUMBER: PCT/US00/22350

PRIOR APPLICATION NUMBER: 60/148,759

PRIOR FILING DATE: 1999-08-16

NUMBER OF SEQ ID NOS: 61

SEQ ID NO 40

LEASTWARE: PatentIN Ver. 2.0

SEQ ID NO 40

LEASTWARE: ABSENTING TO 10 NOS: 61

SEQ ID NO 40

LEASTWARE: ABSENTING TO 10 NOS: 61

SEQ ID NO 40

LEASTWARE: ABSENTING TO 10 NOS: 61

CONTRACTOR 10 NOS: 61
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Pred. No. 26;
3; Mismatches 7;
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US-09-833-245-2260
, Sequence 2260, Application US/09833245
, Publication No. US20040010134A1
, GENERAL INFORMATION:
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Best Local Similarity 37.5%;
Matches 15; Conservative
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ORGANISM: Homo sapiens
US-09-768-826-40
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-09-768-826-40
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Query Match 38.9%; Score 54.5; DB 14; Length 566; Best Local Similarity 37.5%; Pred. No. 32; Matches 15; Conservative 3; Mismatches 7; Indels 15
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PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/279,995
PRIOR APPLICATION NUMBER: 60/294,899
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-19
PRIOR PELICATION NUMBER: 60/299,027
PRIOR PELING DATE: 2001-06-19
PRIOR PELING DATE: 2001-06-19
PRIOR PLING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR PLING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PLING DATE: 2001-03-03
PRIOR PLING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 370
SOFTWARE: PALENTIN VAINBER: 60/275,578
PRIOR PLING DATE: 2001-03-13
SENOTHARES DATES
PRIOR PLING DATE: 2001-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 188, Application US/10093463
Publication No. US20030208039A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Padigaru, Muralidhara
APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Ramesh
APPLICANT: Rekuda, Ramesh
APPLICANT: Pochart, Pascal
APPLICANT: Zhong, Mei
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Smithson, Glennda
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Pena, Carol
Burgess, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zerhusen, Bryan
Tchernev, Velizar
Gangolli, Esha
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Gorman, Linda
Spaderna, Steven
Voss, Edward
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Gerlach, Valerie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-093-463-190
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APPLICANT: Acturajan, Meera
APPLICANT: Miller, Charles
APPLICANT: Taupier, Raymond J. Jr.
TITLE OF INVENTION: No. US20030208039A1e1 Antibodies that Bind to Antigenic Polypepti
TITLE OF INVENTION: No. US20030208039A1e1
TITLE OF INVENTION: Encoding The Antigens, and Methods of Use.
TITLE OF INVENTION: 21402-30A (Cura 590AT)
CURRENT APPLICATION NUMBER: US/10/093,463
CURRENT FILING DATE: 2001-04-14
PRIOR APPLICATION NUMBER: 60/283,675
PRIOR APPLICATION NUMBER: 60/283,675
PRIOR FILING DATE: 2001-04-14
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/274,281
PRIOR APPLICATION NUMBER: 60/274,101
PRIOR FILING DATE: 2001-03-08
PRIOR PRIOR FILING DATE: 2001-03-08
PRIOR PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/274,101
PRIOR PRIOR FILING DATE: 2001-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                            NAME/KEY: SITE
1 LOCATION: (270)
2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-768-826-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

38.9%; Score 54.5; DB 9; Length 565;
Best Local Similarity 37.5%; Pred. No. 31;
Matches 15; Conservative 3; Mismatches 7; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GDF-----AQAAQQLW-----LALRALGRPLPTSH 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 190, Application US/10093463
Publication No. US20030208039A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/304,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Padigaru, Muralidhara
APPLICANT: Shenoy, Suresh
APPLICANT: Rekuda, Ramesh
APPLICANT: Rekuda, Ramesh
APPLICANT: Pochart, Pascal
APPLICANT: Zhong, Mei
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Gasman, Stacie
APPLICANT: Boldog, Ferenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burgess, Catherine
Liu, Xiaohong
Spyrek, Kimberly
Gorman, Linda
Spaderna, Steven
Voss, Edward
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Zerhusen, Bryan
Tchernev, Velizar
Gangolli, Esha
Vernet, Corine
Pena, Carol
                                 NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58
LENGTH: 565
TYPE: PRT
ORGANISM: Homo sapiens
      PRIOR FILING DATE: 1999-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malyankar, Uriel
Anderson, David
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APPLICANT: Anderson, bavid
APPLICANT: Anderson, bavid
APPLICANT: Anderson, bavid
APPLICANT: Taugler, Charles
APPLICANT: Taugler, Charles
APPLICANT: Taugler, Charles
APPLICANT: Taugler, Charles
APPLICANT: Taugler, Raymond
ITILE OF INVENTION: No. USZ0032030401
ITILE OF INVENTION: Benciding The Anti-gens, and Methods of Use.
ITILE APPLICANTON NUMBER: 0203-06-4
PRIOR APPLICANTON NUMBER: 0203-06-4
PRIOR APPLICANTON NUMBER: 0201-06-4
PRIOR APPLICANTON NUMBER: 0201-06-61
PRIOR APPLICANTON NUMBER: 0203-06
PRIOR PRIOR
                                                                                                                                                                                                                                                 Burgess, Catherine
Liu, Xiaohong
Spytek, Kimberly
Gorman, Linda
Spaderna, Steven
Vass, Bdward
Walyankar, Uriel
Anderson, David
                                                                                                                                                  Zerhusen, Bryan
Tchernev, Velizar
Gangolli, Esha
Vernet, Corine
Pena, Carol
          Mezes, Peter
Smithson, Glennda
Guo, Xiaojia
Gerlach, Valerie
Casman, Stacie
Boldog, Ferenc
Li, Li,
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CGGANISM: Homo sapiens
US-10-093-463-192
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38.9%; Score 54.5; DB 14; Length 647;
Best Local Similarity 37.5%; Pred. No. 36;
Matches 15; Conservative 3; Mismatches 7; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 GBFSCEPPLIARHTORLWVLEGORATLRCRALGDPAPTMH 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 192, Application US/10093463 Publication No. US20030208039A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Padigaru, Muralidhara
APPLICANT: Shenoy, Suresh
APPLICANT: Kekuda, Ramesh
APPLICANT: Gusev, Vladimir
APPLICANT: Pochart, Pascal
APPLICANT: Zhong, Mei
Anderson, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-10-093-463-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-093-463-192
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Search completed: November 10, 2004, 16:36:06 Job time: 27.0417 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

November 10, 2004, 11:36:51; Search time 5.45833 Seconds (without alignments) 475.942 Million cell updates/sec Run on:

US-10-092-750-22 140 1 ARGDFAQAAQQLWLALRALGRPLPTSH 27

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ription fac			O1	adenylate cyclase	hypothetical prote	lycopene cyclase -	lymphotoxin C1 pre	probable D-alanyl-	oxidoreductase - S	anthranilate synth	ATP-dependent DNA	hypothetical prote	hypothetical prote	NADH dehydrogenase	BPLF1 protein - hu	acetyltransferase,	/Ycio/YrdC	FixI protein - Rhi	Fix11 copper trans	Q	DNA maturase B - p		glycine-tRNA ligas	hypothetical prote	ase	ble rhamno	g	probable retroelem
SUMMARIES	CI	A48085	A54164	σ,	A54962	T10905	A84212	54	A36379	H83265	T34919	T46852	E83226	C64386	Th.	F75387	QQBE8	E87350	D87669	C32052	C95344	AE0289	JVBPB3	T06672	T48850	T05590	AC2986	9829	875212	8448
	DB	2	(1	~	~	N	N	N	N	N	N	N	~	~	N	0	Н	~1	7	N	7	N	-	N	N	~1	~	0	N	7
	Length	927	1133	1139	1141	352	904	410	72	476	347	0	Н	109	336	444	3149	312	325	757	757	370	586	1067	1067	383	428	460	709	1402
de	Query Match	92.1	92.1	53.6	53.6	36.4	36.1	Ŋ.	34.6	34.6	4	4.	4.	33.9	ω.	ω.	ω.	ω.	ω.	ω.	ω,	'n.	ω,	'n	ω,	ά.	ď	ď	32.9	
	Score	129	129	75	75	51	50.5	49	48.5	48.5	48	48	48	47.5	47.5	47.5	47.5	47	47	47	47	46.5	46.5	46.5	46.5	46	46	46	46	46
	Result No.		7	m	4	D	G	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

alkaline phosphata	hypothetical prote	GGDEF family prote	hypothetical prote	cellobiose phospho	cellobiose phospho	hypothetical prote	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	neural cell adhesi	hypothetical prote	phage lysis protei	chpB protein - Pse	Ra-reactive factor
S74570	T49282	G82209	T00257	AD1410	AC1786	H84095	B71340	D87534	G81654	A83271	T30581	E75463	YVBPF6	T30314	154763
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326	609	976	1386	100	100	322	337	407	602	741	1197	199	220	343	669
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32.	32	32	32	32	32,	32.	32	32	32	32.1	32	31	31	31	31
45.5	45.5	45.5	45.5	45	45	45	45	45	45	45	45	44.5	44.5	44.5	44.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

A48085 transcript C;Species: C;Accessio C;Accessio R;Tontonoz Mol. Cell. A;Atle: A	A48085 Libranscription factor ADD1 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 04-Sep-1998 C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 04-Sep-1998 C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 04-Sep-1998 C;Date: 26-May-1994 #sequence_revision 36-May-1994 #text_change 04-Sep-1998 R;Tontconaz, P: Kim, J.B.; Graves, R.A.; Spiegelman, B.M. Mol. Cell. Biol. 13, 4753-4759, 1993 A;Title: anovel helix-loop-helix transcription factor associated with adipocyte de A;Accession: A48085 A;Residues: 1-927 < TON-
transcript C,Species: C,Date: 26 C,Accessio R,Tontonoz Mol. Cell. A,Tille: A	orion factor ADD1 - rat 15. Rattus norvegicus (Norway rat) 15. May-1994 #sequence_revision 26.May-1994 #text_change 04.Sep-1998 16. May-1994 #sequence_revision 26.May-1994 #text_change 04.Sep-1998 16. 19. 19. 19. 49. 19. 19. 19. 19. 19. 19. 19. 19. 19. 1
C;Species: C;Date: 26 C;Accosio R;Tonconcs Mol. Cell. A;Title: A	Rattus norvegicus (Norway rat) 6-May-1994 #sequence_revision 26-May-1994 #text_change 04-Sep-1998 con: A48085 22, P.; Kim, J.B.; Graves, R.A.; Spiegelman, B.M. 22, P.; Kim, J.B.; Graves, R.A.; Spiegelman, B.M. ADDI: a novel helix-loop-helix transcription factor associated with adipocyte de number: A48085; MUID:93330269; PMID:8336713 con: A48086 cb. Type: mRNA se: 1-927 <ton></ton>
C;Date: 26 C;Accessio R;Tonconoz MOI. Cell. A;Title: A A;Referen A;Accessio	16-May-1994 #sequence_revision 26-May-1994 #text_change 04-Sep-1998 20. P. 18.10 J. B. 1 Graves, R.A.; Spiegelman, B.M. 21. P. 18.10 J. 13. 4753-4759, 1993 32. P. 18.10 J. 13. 4753-4759, 1993 33. Dabl: a novel helix-loop-helix transcription factor associated with adipocyte denomber: A48085; MulD:93330269; PMID:8336713 33. Pareliminary 45. Trons 55. Trons 56. Trons 56. Trons
C;Accessio R;Tontonoz Mol. Cell. A;Title: A A;Referenc A;Accessio	on: A48085 P.; Kim, J.B.; Graves, R.A.; Spiegelman, B.M. A101. 13, 4753-4759, 1993 ADD1: a novel helix-loop-helix transcription factor associated with adipocyte descentione number: A48085; MUID:93330269; PMID:8336713 On: A48086 I preliminary e type: mRNA e type: mRNA ss: 1-927 <ton></ton>
R; Tontonoz Mol. Cell. A; Title: A A; Referenc A; Accessio	12, P.; Kim, J.B.; Graves, R.A.; Spiegelman, B.M. 1. Biol. 13, 4753-4759, 1993 ADDI: a novel helix-loop-helix transcription factor associated with adipocyte de novel helix-loop-helix transcription factor associated with adipocyte de number: A48085; MUD:93330269; PMID:8336713 On: A48085 preliminary to type: mRNA se: 1-927 <ton></ton>
MO1. Cell. A;Title: A A;Referenc A;Accessio	Biol. 13, 4753-4759, 1993 ADD1: a novel helix-loop-helix transcription factor associated with adipocyte de nor number: A48085; MulDi93330269; PMID:8336713 On: A48085 On: preliminary e type: mRNA ss: 1-927 <ton></ton>
A,Title: A A,Referenc A,Accessio	ADD1: a novel helix-loop-helix transcription factor associated with adipocyte descendment A48085; MUD193330269; PMID18336713 con: A48085 preliminary te type: mRNA ss: 1-927 <ton></ton>
A, Referenc A, Accessio	ice number: A48085; MUID:93330269; PMID:8336713 On: A88086 Preliminary te type: mRNA Se: 1-927 <ton></ton>
A,Accessio	on: A48085 preliminary e type: mRNA se: 1-927 <ton></ton>
	preliminary e type: mRNA ss: 1-927 <ton></ton>
A;Status:	.е Lype: mRNA 58: 1-927 <ton></ton>
A;Molecule	. 1-927 <ton></ton>
A; Residues	
A, Cross-re	A;Cross-reterences: GB:L16995
C;Superfam	C, Superfamily: sterol regulatory element binding protein
C; Keywords	C,Keywords: leucine zipper
Query Ma	Query Match 92.1%; Score 129; DB 2; Length 927;
Best Local	ocal Similarity 92.5%; Fred. NO. 1.18-10; 3 25; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
λö	1 ARGDFAQAQQUMLALRALGRPLPTSH 27
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RESULT 2

A54164
Sterol regulatory element-binding protein 1 - Chinese hamster
Sterol regulatory element-binding protein 1 - Chinese hamster
(.Species: Cricetulus griseus (Chinese hamster)
(.Species: Cricetulus griseus (Chinese hamster)
(.Space: 07-Jil-1995 #sequence_revision 07-Jil-1995 #text_change 09-Jul-2004
(.Sacossion: A54164
A. Hang, X.; Evans, M.J.; Ho, Y.K.; Goldstein, J.L.; Brown, M.S.
A. Pitle: Assignment of the membrane attachment, DNA binding, and transcriptional activat)
A. Reference number: A54164
A. Status: prollminary
A. Mollimary
A. Molecule type: mRNA
A. Residues: 1-1133 <-SAT>
A. Residues: 1-1133 <-SAT>
A. Residues: 1-1133 <-SAT>
A. Status: prollminary
A. Residues: 1-1134 Status: prollminary
C. Superfamily: sterol regulatory element binding protein

Query Match 92.1%; Score 129; DB 2; Length 1133; Best Local Similarity 92.6%; Pred. No. 1.4e-10; Matches 25; Conservative 2; Mismatches 0; Indels

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Gaps ö

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A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1139 <YAN>

Query Match Best Local Similarity

Matches

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R;Coudart-Cavalli, M.P.; Sismeiro, O.; Danchin, A.

Bibmitted to the EMBL Date Library, January 1998
A;Description: Bifunctional structure of two adenylyl cyclases from the myxobacterium Sti
A;Reference number: Z17211
A;Accession: T10905
A;Accession: T10905
A;Accession: T10905
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-552 <COU>
A;Residues: 1-552 <COU>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: involved in cAMP synthesis
C; Superfamily: sensory transduction system regulatory protein; response regulator homolog
C; Keywords: phosphorus-oxygen lyase
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Cipate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
Cipate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
Cipate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Danlablas, C.J.; Dennist, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liz
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT:Q9HRU7; GB:AE004437; NID:g10580137; PIDN:AAG19061.1; GSPDB:GR-C;Genetics:
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lycopene cyclase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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36.4%; Score 51; DB;
Best Local Similarity 55.0%; Pred. No. 9.3;
Matches 11; Conservative 1; Mismatches
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36.1%; Score 50.5; D
Best Local Similarity 54.5%; Pred. No. 28;
Matches 12; Conservative 3; Mismatches
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A;Molecule type: DNA
A;Residues: 1-410 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A84212
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N;Alternate names: basic-helix-loop-helix-leucine zipper transcription factor SREBP-2
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: A49397; A54962
R;Hua, X.; Yokoyama, C.; Wu, J.; Briggs, M.R.; Brown, M.S.; Goldstein, J.L.; Wang, X.
A;Hua, X.; Sokoyama, C.; Wu, J.; Briggs, M.R.; Brown, M.S.; Goldstein, J.L.; Wang, X.
A;Hitle: SREBP-2, a second basic-helix-loop-helix-leucine zipper protein that stimulates
A;Reference number: A49397; MUID:94089681; PMID:7903453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 1-1141 <HUNA
A,Residues: 1-1141 <HUNA
A,Cross-references: UNIPROT:Q12772; GB:U02031; NID:g451329; PIDN:AAA50746.1; PID:g451330
A,Experimental source: HeLa cells
A,Note: sequence extracted from NCBI backbone (NCBIP:140987)
B,Yang, J,; Sato, R,; Goldstein, J.L.; Brown, M.S.
Genes Dev. 8, 1910-1919, 1994
A,Title: Sterol-resistant transcription in CHO cells caused by.gene rearrangement that the A,Reference number: A54962; MUID:95047343; PMID:7958866
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Comment: Under conditions of sterol depletion, this membrane-bound transcription facto
                                                                                                                                                                                             R;Yang, J;; SaTC, R.; Goldstein, J.L.; Brown, M.S.
Genes Dev. 8, 1910-1919, 1994
A;Title: Sterol-resistant transcription in CHO cells caused by gene rearrangement that
A;Reference number: A54962; MUID:95047343; PMID:7958866
A;Accession: B54962
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0
                                                           sterol regulatory element binding protein 2 precursor - Chinese hamster C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004 C;Accession: B54962
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C;Species: Stigmatella aurantiaca
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1139;
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C;Superfamily: sterol regulatory element binding protein
C;Keywords: DNA binding; membrane protein; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 53.6%; Score 75; DB 2; Length 113 ll Similarity 65.4%; Pred. No. 0.0097; 17; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q60429; GB:U12330
A;Note: 493 Ser was also found
C;Superfamily: sterol requlatory element binding protein
C;Keywords: DNA binding; membrane protein
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A;Gene: GDB:SREBF2; SREBF2 A;Cross-references: GDB:273625

RESULT 5

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Genetics:

us-10-092-750-22.rpr

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authorsal antiques (BC 4.1.3.27) component I [similarity] - Rhodobacter sphaeroides anthranlate synthase (BC 4.1.3.27) component I [similarity] - Rhodobacter sphaeroides C;Species: Rhodobacter sphaeroides C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004 C;Accession: T46852 B;Assion: 13, 525-538, 1999 A;Aitle: Multiple chromosomes in bacteria. The Yin and Yang of trp gene localization in FA;Accession: T46852 A;Accession: T46852 A;Access
C;Species: Streptcomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T34919
A;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A;Accession: T34919
A;Accession: T34919
A;Accession: T34919
A;Accession: T34919
A;Retue: preliminary; translated from GB/EMBL/DDBJ
A;Residues: Dreliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-347 - CLL
A;Residues: 1-347 - CLL
A;Resperimental source: strain A3(2)
A;Resperimental source: strain A3(2)
A;Gene: SCOEDB:SC3F7.13
C;Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
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C;Species: Pseudomonas aeruginosa
C;Accession: E83226
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, ..., Lory, S.; Olson, M.V.
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A,Reference number: A82950; MUID:20437337; PMID:10984043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 2;
Pred: No. 25;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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C,Superfamily: anthranilate synthase component I
C,Keywords: carbon-carbon lyase; oxo-acid-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ARGDFAQAAQQLWLALRALGRPLP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 ATVSEKLWGALRIDSRPVLTRH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AQAAQQLWLALRALGRPLPTSH 27
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Best Local Similarity 45.5%;
Matches 10; Conservative
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Best Local Similarity 50.0
Matches 12; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-712 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: trpE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable D-alanyl-D-alanine carboxypeptidase PA3047 [imported] - Pseudomonas aeruginosa CiSpecies: Pseudomonas aeruginosa CiSpecies: Pseudomonas aeruginosa CiSpecies: Pseudomonas aeruginosa CiDate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 CiAccession: #83265

Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bristover, C.K.; Pham, X.Q.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jurer, 406, 959-964, 2000

A; Lordy, S.; Olson, M.V.
A; Reference number: A82950; MUD:20437337; PMID:10984043 an opportunistic pathor A; Accession: H83265
A; Residues: Preliminary
A; Residues: 1-476 <STO.
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A;Experimental source: strain PAO1
A;Genetics: PA3047
C;Superfamily: D-alanyl-D-alanine carboxypeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
343379

A36379

Lymphotoxin C1 precursor - mouse (fragment)

C,Species: Mus musculus (house mouse)

C,Species: Mus musculus (house mouse)

C,Species: Mus musculus (house mouse)

C,Accession: A36379

R,Weil, D.; Brosset, S.; Dautry, F.

Mol. Cell. Biol. 10, 5865-5875, 1990

A;Title: RN processing is a limiting step for murine tumor necrosis factor beta express

A;Reference number: A36379

A;Accession: A36379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 72;
                                                                                                                                                                                              Query Match
35.0%; Score 49; DB 2; Length 410;
Best Local Similarity 46.2%; Pred. No. 21;
Matches 12; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
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Pred. No. 29;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                    1 ARGDFAQAAQQLWLALRALGRPLPTS 26
                                                                                                                                                                                                                                                                                                                                                                                                60 ARG----CAEQVWIDVRAYIGPOPIS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | || ||||||: || || : : |
| ADGDDAQAAQRVVRQWLARKGITAP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GDFAQAAQQLWLALRALGRPLPTSH 27
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T34919
oxidoreductase - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 48.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 48.0%;
Matches 12; Conservative
               R
           A, Experimental source: strain C, Genetics: A, Gene: DR0801 A, Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
Residues: 1-72 < WBI>
A;Cross-references: GB:M60586
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A, Experimental source: strain PAO1

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C,Accession: F75387
R,Mhite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F. M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mab. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 1 C_iSuperfamily: NADH dehydrogenase (ubiquinone) 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPROT:Q9RU92; GB:AE001994; GB:AE000513; NID:g6459259; PIDN:AAF11067
                                                                                                                                                                                                                                                                                                                                                          A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: F75387
                                                                                                                                   C,Species: Déinococcus radiodurans
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                              NADH dehydrogenase I, F subunit - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.9%; Score 47.5; Dilarity 45.5%; Pred. No. 38; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: November 10, 2004, 12:29:28 Job time: 7.45833 secs
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
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RiNg, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Maddocks, D.G.; Jable Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
Aphathors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MJID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R. Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
4, Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A. Authors: Raine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A. Arfalter Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii, A.Reference number: A64300; MuID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT:Q9HPY8; GB:AE004437; NID:g10580915; PIDN:AAG19729.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: UNIPROT:Q58103; GB:U67516; GB:L77117; NID:g2826307; PIDN:AAB98686.1.
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C,Species: Halobacterium sp. NRC-1
C,Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Methanococcus jannaschii
.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                            Gaps
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Best Local Similarity 44.4%; Pred. No. 9.4;
Matches 12; Conservative 5; Mismatches 9; Indels
                                                                                                                               Query Match
34.3%; Score 48; DB 2; Length 712;
Best Local Similarity 46.7%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ypothetical protein MJ0691 - Methanococcus jannaschii
C;Genetics:
A;Gene: recQ; PA3344
C;Superfamily: recQ protein; recQ helicase homology
                                                                                                                                                                                                                                                                                                                                       520 ASAASQLVRSEEREMWEALRALRRKLAEEH 549
                                                                                                                                                                                                                                                                         6 AQAAQQL-----WLALRALGRPLPTSH 27
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Molecule type: DNA
Residues: 1-336 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: C64386
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194 AAADALAEALQNWMELRALG-PEPAS 218

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Gaps

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DB 2; Length 444; Indels Н

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 10, 2004, 11:27:01 ; Search time 28.5417 Seconds (without alignments) 525.871 Million cell updates/sec Run on:

US-10-092-750-22

140 1 ARGDFAQAAQQLWLALRALGRPLPTSH 27 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1	ption	O6pj36 homo sapien	21 hom	homo sa	ens s	^	рошо	38 hon	sus scr	88 BUB	homo sa	Aah63281 homo sapi	rattus	Q60416 cricetulus	~	Q9wtn3 mus musculu	Q8c733 mus musculu	Aah56922 mus muscu	Q90zm5 gallus gall	Q60429 cricetulus	Q12772 homo sapien	Aah56158 homo sapi	S Ome		Q8pmm2 xanthomonas	Q6gq26 xenopus lae		Q8k3c4 mus musculu	29 m	Q73rm1 treponema_d	9	Ofip16 homo sapien
SUMMARIES	D	690	AAH23621	Q8TAK9	Q7YS02	SRE1 HUMAN	Q6PFW7	AAH57388	Q6RIB9	AAS18238	Q6P4R7	AAH63281	SRE1_RAT	SRE1_CRIGR	Q99JK7	SRE1_MOUSE	Q8C733	AAH56922		SRE2_CRIGR	5	AAH56158	Q86V36	092502	Q8 PMM2	Q6GQ26	QBOXUB	Q8K3C4	BAC38259	Q73RM1	AAS10565	QGIPL6
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AAH71866 AAH27475	Q6PK41 AAH07718 Q6PJG9	AAH15581 Q8DGR8 Q8PAX0	FMT_SHEON CYAB_STIAU Q99PX4	Q73YT0 AAS04192 Q9VIG1
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ALIGNMENTS

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	ULT 1 36 665036 665036 65-0711-2004 65-0711-2004 65-0711-2004 8RBB1 prote Name=SRBB1; Name=SRB1; Name=SRB	PRELIMINARY; (TrEMBLrel. 2' (TrEMBLrel. 2' (TrEMBLrel. 2' in (Fragment)	(Human). stazoa, Chord heria, Primal 106; 10, Feingold 11, Zeeberg B. 2057; Fubmed= 12, Usdin T. Marusha H., Norley K.C., Worley K.C., Worley K.C., Muzny D.N., Touchman A., Youn 11, Skalska 12, Grimwood 11, Skalska 14, Skalska 14, Skalska 16, Grimwood 17, Grimwood 17, Grimwood 18, Skalska 18, Skalska 11, Skalska 11, Skalska 11, Skalska 12, Grimwood 11, Skalska 14, Skalska 16, Grimwood 17, Grimwood 18, Skalska 19, Apht3621 11, Skalska 11, Skalska 11, Skalska 12, Grimwood 13, Grimwood 14, Skalska 16, Grimsood 17, Grimwood 18, Skalska 19, Grimsood 10, Grimsood 10, Grimsood 11, Apht3621 11, Apht362 11, Apht362	Conservative

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RESULT 2 AAH23621

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PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
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EMBL, BC026962, AAH26962.1;
Hypothetical protein.
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Best Local Similarity 100.0'
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A tausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Thelton B.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Thelton B.K., Muzny D.M., Gaergren B.J., Lu X., Gibbs R.A.,

A Thelton B.K., Muzny D.M., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Brodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Thelton B.K., Marra M.A.,

A Thelton B.K., Marra M.A.,

A Thelton B.K., Marra M.A.,

Brones S.J., Marra M.A.,

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023621; -.
NON TER 1
SEQÜENCE 686 Aa; 74450 MW; 7439AF380530A6D2 CRC64;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment)
Homo sapiens (Human)
                                                                                                                                                               Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Best Local Similarity 100.0%;
Matches 27; Conservative 0
                                                                                                                                  02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                              SREBF1 protein (Fragment). SREBF1.
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RESULT 3 Q8TAK9

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TISSUBE-Gervical carcinoma;
MEDLINE-940C6541; PubMede-6402897;
YOKOYAMA C., Wang X., Briggs M.R., Admon A., Wu J., Hua X.,
Goldstein J.L., Brown M.S.;
"SREBP-1, a basic-helix-loop-helix-leucine zipper protein that
controls transcription of the low density lipoprotein receptor gene.";
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P36956; 016062;
01-UNN-1994 (Rel. 29, Created)
01-UNN-1994 (Rel. 29, Last sequence update)
01-OCT-2004 (Rel. 29, Last annocation update)
01-OCT-2004 (Rel. 45, Last annocation update)
10-OCT-2004 (Rel. 29, Last annocation update)
10-OCT-2004 (Rel. 20, Last annocat
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Sterol regulatory binding transcription factor i (Fragment).
Name=SREBP-1c;
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Palin M.F., Beaudry D., Murphy B.D.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
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750 AA; 80631 MW; 6F2E49703C886ED3 CRC64;
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                                                                                                          100.0%; Score 140; DB 2;
100.0%; Pred. No. 6.9e-11;
ative 0; Mismatches 0;
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EMBL; S66168; AAB28523.1; -.
DBB; IAM9; X-raq, A/B/C/D=319-400.
TRANSFAC; T01556; -.
Genew; HGNC:11289; SREBFI.
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        Exrocture 6:661-672 (1998).

Structure 6:661-672 (1998).

-!-FUNCTURE 6:661-672 (1998).

-!-SUBLORY: Forms a tight complex with Experiment of genes for sterol biosynthesis and the LDL receptor gene.

-!-SUBLORY: Forms a tight complex with SGAP in the Ex membrane.

Efficient DNA binding of the soluble transcription factor fragment requires dimerization with another bHLH protein.

-!-SUBCEDIULIAR LOCATION: Integral membrane protein that moves from the endoplasmic reticulum to the Golgi in the absence of sterols.
                                                                                                                                                                                                                                                                                                                                         MEDLINE=98298442; PubMed=9634703;
Parraga A., Bellsolell L., Ferre-D'Amare A.R., Burley S.K.;
"Co-crystal structure of sterol regulatory element binding protein la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         white fat, and muscle.

PTM: Under sterol-depleted conditions, SREBPs are cleaved sequentially by site-1 and site-2 protease. The first oleavage occurs within the luminal loop and is directly regulated by sterols. The second cleavage by site-2 protease occurs within the first transmembrane stretch and liberates the soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription factor. Cleavage by the cysteine proteases, caspase-3 and caspase-7, is induced during apoptosis, independent of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoid=P36956-3; Sequence=VSP 002149, VSP 002150;
TISSUE SPECIFICITY: Expressed in a wide variety of tissues, most abundant in liver and adrenal gland. In fetal tissues lung and liver shows highest expression. Isoform SREBP-1C predominates in liver, adrenal gland and ovary, whereas SREBP-1A predominates in hepatoma cell lines. Both isoforms are found in kidney, brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sterol levels. MISCELLANBOUS: SREBPS have to be in a complex with the cleavage-activating protein (SCAP) to move to the Golgi and be cleaved by
                                                 TISSUB=Fetal brain;
MEDLINE=9525936; PubMed=7759101;
MEDLINE=9525936; PubMed=7759101;
"Structure of the human gene encoding sterol regulatory element
binding protein-1 (SREBF1) and localization of SREBF1 and SREBF2 to
chromosomes 17p11.2 and 22q13.";
Genomics 25:667-673(1995).
                                                                                                                                                                                CHARACTERIZATION, AND MUTAGENESIS.
MEDUINE-96215341; PubMed-8626610;
Hua X., Sakai J., Brown M.S., Goldstein J.L.;
"Regulated cleavage of sterol regulatory element binding proteins requires sequences on both sides of the endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       site-1 protease.
SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
Name=SREPB-1A;
                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 319-394.
                                SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=SREBP-1B;
Isold=P36956-2; Sequence=VSP_002150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P36956-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                       membrane.";
J. Biol. Chem. 271:10379-10384(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U00968; AAC50051.2; -.
EMBL; S66167; AAB28522.2; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=SREBP-1C;
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MIM), 184756; ...
GO; GO:0005638; C:endoplasmic reticulum membrane; TAS.
GO; GO:0005635; C:nuclear membrane; TAS.
GO; GO:0003702; F:RNA polymerase II transcription factor acti. . .; TAS.
GO; GO:0006357; P:Inipid metabolism; TAS.
GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; TAS.
InterPro; IPRO0102; HLH, basic.
Pham; PPO0010; HLH; 1.
SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleavage (by Caspase-3 and caspase-7) (By similarity).
Cleavage (by S2D) (By similarity).
Cleavage (by S1P) (Probable).
MDEPPREMALEQALGEPCDLDAALLIDI -> MDCTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFLHEATARLMAGASPTRTHQLLDRSLRRRAGPGGKGGAVA
ELEPRPTREHAEALLLASCYLDEPGFLSAPGQRVGMLAEAA
RTLEKLGDRRLLHDCQQMLMRLGGGTTVTSS -> LMDVLT
SESAWALPQHLGKGPSPSGSHKVPGMRGMD (in
                                                                                                                                                                                                                                          PROSITE; PSS0888, HLM; 1.
3D-structure; Activator; Alternative splicing; Cholesterol metabolism; Direct protein sequencing; Darby Endoplasmic reticulum; Golgi stack; Lipid metabolism; Nuclear protein; Transcription regulation; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isoform SREBP-1B and isoform SREBP-1C). /FTId=VSP_002150.
S->A: No effect on the cleavage by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sterol-regulated procease.
D-A: No effect on the cleavage by the sterol-regulated procease.
G-A: No effect on the cleavage by the sterol-regulated procease.
M-A: No effect on the cleavage by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helix-loop-helix motif (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TŘANŠCRIPTIONAL ACTIVATION (ACIDIC).
Pro/Ser-rich.
Basic motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sterol-regulated protease.
D-A: No effect on the cleavage by sterol-regulated protease.
S-A: No effect on the cleavage by sterol-regulated protease.
D-A: No effect on the cleavage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D->A: Abolishes the cleavage by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R->A: Abolishes the cleavage by the
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Gly/Pro/Ser-rich.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lumenal (Potential).
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Best Local Similarity
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Homo sapiens (Human)
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                                                                                                                      SEQUENCE FROM N.A.
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hishe F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Frange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Frange C.,
Brownstein M.J., Wokernan K.J., Malek J.A., Gunaratne P.H.,
Broak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Alchards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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100.0%; Pred. No. 1e-10;
iive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                     05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Sterol regulatory element binding transcription factor 1.
Name-SRBBF1, (Human).
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Sterol regulatory element binding transcription factor 1.
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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0; Mismatches
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                                                  1 ARGDFAQAAQQLWLALRALGRPLPTSH 27
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Best Local Similarity 100.0
Matches 27; Conservative
27; Conservative
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                                                                                                                                                                                                                                                Q6PFW7;
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  Matches
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AAH57388
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**X STANDENCELLES:

**A STANDENCELLES:

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**A STANDENCELLES:

**A STANDENCELLES:

**A Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

**A Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

**A Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

**A Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

**A Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

**A Altachul S.F., Zeeberg B., Bernaldo M.F., Casavant T.L., Scheetz T.E.,

**A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

**A Ray S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**A Park J., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

**A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**A Northey W. Touchman J.W., Green E.D., Dickson M.C.,

**A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

**A Northe W.H., M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

**A Dones S.J., Marra M.A.,

**A Dones S.J.,

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Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Butaleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Sus.
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GGRIB9. 05-UDL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Adipocyte determination and differentiation-dependent factor 1.
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PROSITE; PS00213; LIPOCALIN; UNKNOWN 1.
SEQUENCE 1151 AA; 121501 MW; F9AEA7FCAF831F2D CRC64;
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TISSUE=Liver;

Li C., Meng H., Zhao W., Pan Y.;

Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AX496867; AAS18238.1; -.

InterPro; IPR001092; HLH basic.

InterPro; IPR000566; Lipocln_cytFABP.

SMART; SM00353; HLH; 1.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
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Best Local Similarity 100.0%;
Matches 27; Conservative 0
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100.0%; Score 140; DB 2; Length 1151;

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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                 SEQUENCE FROM N.A.
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AAH63281;
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WEDINE=2238257, PubMed=12477932;

WETAUSDETE R. D. Peingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

A Didchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Didchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Willalon D.K., Mazny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ray Stalska U., Smailus D.E., Schnerch A., Schein J.E.,

Ray Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Bukaryota; Metazomi.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Adipocyte determination and differentiation-dependent factor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 140; DB 2; Length 1151; 100.0%; Pred. No. 1.1e-10; cive 0; Mismatches 0; Indels 0
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li C., Meng H., Zhao W., Pan Y.; "Pig ADD1 gene cloning and expression."; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AY496867; AAS18238.1; "SEQUENCE 1151 AA; 121501 MW; F9AEA7FCAF831F2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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              100.0%; Pred. No. 1.1e-10; ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 27; Conservative
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Li C., Meng H.
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AAS18238;
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Q6P4R7;
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C064R7
C067R8
AC C067R8
DDT C05-JU
DDT C06-JU
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11D AAS1

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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
TISSUE=Brain;
Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0623B1; AAH632B1.1; -.
InterPro; IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
SWART; SM00353; HLH; 1.
PROSITE; PS50888; HLH; 1.
SEQUENCE 1177 AA; 124633 MW; 4E78AA235B8BC320 CRC64;
                                                                                                                                                                                                                                                                                        124633 MW; 4E78AA235B88C320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC063281; AAH63281.1; -.
SEQUENCE 1177 AA; 124633 MW; 4E78AA235B88C320 CRC64;
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-2004 (TrEMBirel, 27, Created)
02-MAR-2004 (TrEMBirel, 27, Last sequence update)
02-MAR-2004 (TrEMBirel, 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 140; DB 2; 100.0%; Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1177 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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RESULT 12

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496
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427
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ID SRE1 CRIGR
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Best Local Si
Matches 25;
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Xim J.B., Spotts G.D., Halvorsen Y.D., Shih H.M., Ellenberger T.,

Xim J.B., Spotts G.D., Halvorsen Y.D., Shih H.M., Ellenberger T.,

Towle H.C., Spiegelman B.M.;

Towle H.C., Spiegelman B.M.;

"bual DNA binding specificity of ADDI/SREBPI controlled by a single
amino acid in the beasto helix-loop-helix domain.";

MOI. Cell. Biol. 15:3582-5588 (1955).

"PUNCTION: Transcriptional activator that binds to the sterol
regulatory element 1 (5RE-1) (5'-ATCACCCCAC-3'). Has dual sequence
specificity, binding to both an B-box motif (5'-ATCACCTGA-3') and

to SRE-1 (5'-ATCACCCAC-3'). Regulates the transcription of genes
for sterol biosynthesis and the LDI receptor gene.

STETICIENT DNA binding of the soluble transcription factor fragment
requires dimerization with another bHLM procein.

-!- SUBCELDUAR LOCATION: Integral membrane procein that moves from
the endoplasmic reticulum to the Golgi in the absence of sterols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIGURE 1 The first cleaved sequentially by site-1 and site-2 protease. The first cleavage sequentially by site-1 and site-2 protease. The first cleavage occurs within the luminal loop and is directly regulated by sterols. The second cleavage by site-2 protease occurs within the first transmembrane stretch and liberates the soluble first transmiption fearor. Cleavage by the cystaine proteases, caspase-3 and caspase-7, is induced during apoptosis, independent of sterol levels (By similarity).

MISCELLANGOUS: SREBPS have to be in a complex with the cleavage-activating protein (SCAP) to move to the Golgi and be cleaved by site-1 protease.
                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Adipocyte;
MEDLINE=5330565; PubMed=8336713;
Tontonoz P., Kim J.B., Graves R.A., Spiegelman B.M.;
Tontonoz P., Kim J.B., Oraves R.A., transcription factor associated with adDbi: a novel helix-loop-helix transcription factor associated with adipocyte determination and differentiation.";
Mol. Cell. Biol. 13:4753-4759(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of a mutation in ADD1/SREBP-1 in the spontaneously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P55720-2; Sequence=Not described; IISSUE SPECIFICITY: Expressed predominantly in brown adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BN-Lx/Cub, and SHR/Ola;
MEDLINE=21212663; PubMed=11309661; DOI=10.1007/s003350010273;
Pravenec M., Jansa P., Kostka V., Zidek V., Kren V., Forejt J.
                                                                                                               SRE1_RAT STANDARD; PRT; 1024 AA.
P56720; Q99P16; Q99P17;
30-WAY-2000 (Rel. 39, Created)
38-FBB-2003 (Rel. 41, Last sequence update)
05-UJL-2004 (Rel. 44, Last annotation update)
Sterol regulatory element binding protein-1 (SREBP-1) (Sterol Sterol regulatory)
                                                                                                                                                                                                                                                    regulatory element-binding transcription factor 1) (Adipocyte determination-and differentiation-dependent factor 1) (ADD1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-1013 FROM N.A., AND VARIANT MET-755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
Name=SREBP-1C; Synonyms=ADD1;
IsoId=P56720-1; Sequence=Displayed;
  624 ARGDFAQAAQQLWLALRALGRPLPTSH 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertensive rat.";
Mamm. Genome 12:295-298(2001).
                                                                                                                                                                                                                                                                                                                      Name=Srebfl; Synonyms=Srebpl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=SREBP-1A;
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
-!- CAUTION: Ref.1 sequence is a conceptual translation, many probable
frameshifts were corrected from position 878 onward.
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SWART, SM00353; HLH; 1.
PROSITE; PS50888; HLH; 1.
Activator; Alternative splicing; Cholesterol metabolism; DNA-binding;
Endoplasmic reticulum; Golgi stack; Lipid metabolism; Nuclear protein;
Polymorphism; Transcription regulation; Transmembrane.
DOMAIN
1 453
Cytoplasmic (Potential).
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Cleavage (by S1P) (By similarity).
V -> M (IN SPONTANEOUSLY HYPERTENSIVE RATS).
G -> A (in Ref. 1).
G -> A (in Ref. 1).
D -> H (in Ref. 1).
Missing (in Ref. 1).
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Leucine-tipper (Potential).
Gly/Pro/Ser-rich.
Cleavage (by caspase-3 and caspase-7) (B
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation factor 1)
16-JUL-1998 (Rel. 37, Last annotation factor 1)
17-JUL-1998 (Rel. 37, Release Legistry)
17-JUL-1998 (Rel. 37, Last annotation factor 1)
18-JUL-1998 (Rel. 36, Last annotation factor 1)
18-JUL-1998 (R
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793 793 D -> H (in Ref. 1).
950 Missing (in Ref. 1).
1024 1024
1024 AA, 108826 MW; 29A2D04E5A27404B CRC64;
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EMBL; AF286470; AAG28734.2; ALT_TERM.
EMBL; AF286465; AAG28733.2; -.
HSSP; P36956; LAM9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGD; 69423; Srebfl.
InterPro; IPR001092; HLH_basic.
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nes 25; Conservative
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SEQUENCE FROM N.A.
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NCBI_TaxID=10029;
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866 AA.

PRELIMINARY;

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TRISTING THE STATE OF THE STATE
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TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                           ol-WAR-2001 (TrEMBLrel. 17, Created)
01-MAR-2004 (TrEMBLrel. 17, Last sequence update)
Srebfl protein (Fragment).
Mane-Srebfl;
                                                                                                                                                                                                                          Mus musculus (Mouse)
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SEQUENCE
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Best Local
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                                                   Transcriptional activation domains of sterol regulatory element.

It transcriptional activation domains of sterol regulatory element.

It transcriptional activation domains of sterol regulatory element.

It diding procein-1 (SREB-1) ";

I. J. Biol. Chem. 269:17267-17273 (1994).

I. FUNCTION: Transcriptional activator that binds to the sterol regulatory element 1 (SRE-1) (5'-ATCACCCCAC-3'). Has dual sequence specificity, binding to both an E-box motif (5'-ATCACCTGA-3') and to SRE-1 (5'-ATCACCCCAC-3'). Regulates the transcription of genes for sterol biosynthesis and the IDL receptor gene.

I. SUBCLIDIAN binding of the soluble transcription factor fragment requires dimerization with another bHLH protein.

I. SUBCLIDIAN LOCATION: Integral membrane protein that moves from the endoplasmic reticulum to the Golgi in the absence of sterols.

I. PTM: Under sterol-depleted conditions, SREBPs are cleaved sequentially by site-1 and site-2 protease. The first cleavage occurs within the luminal loop and is directly regulated by sterols. The second cleavage by site-2 protease occurs within the transcription farrance of stretch and liberates the sculuble properse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00353; HLH; 1.
PROSTIP: PSCOBSE; HLH; 1.
Activator; Cholesterol metabolism; DNA-binding; Endoplasmic reticulum; Golgi stack; Lipid metabolism; Nuclear protein;
Transcription regulation; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage (by caspase-3 and caspase-7) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription factor. Cleavage by the cysteine proteases, caspase-3 and caspase-7, is induced during apoptosis, independent of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sterol levels.

-!- MISCELLANBOUS: SREBPs have to be in a complex with the cleavage-activating protein (SCAP) to move to the Golgi and be cleaved by site-1 protease.
-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helix-loop-helix motif (By similarity)
Leucine-zipper (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic (Potential).
TRANSCRIPTIONAL ACTIVATION (ACIDIC).
                       Yang J., Wang X., Evans M.J., Ho Y.K., Goldstein J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).

Gleavage (by S2P) (By similarity)
Cleavage (by S1P) (By similarity)
W; 01A77B09DEDCDAB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.1%; Score 129; DB 1; Length 1133; 92.6%; Pred. No. 3.6e-09;
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Basic motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential
  MEDLINE=94274723; PubMed=8006035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
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PIR; A54164; A54164.
HSSP; P36956; 1AM9.
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518 51
1133 AA;
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                       Sato R., Yar
Brown M.S.;
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RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

B EMBL; BC006051; AAH0651.1; -..

DR GO; GO:0005634; C:nucleus; IDA.

R GO; GO:0003700; F:transcription factor activity; IDA.

R GO; GO:0003700; P:regulation of transcription; IDA.

R GO; GO:0003700; HHH; 1.

R Ffam; PF00010; HHH; 1.
                                                                                                                                                                                                                                                                                                                                             88.6%; Score 124; DB 2; Length 866; 88.9%; Pred. No. 1.4e-08; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                      866 AA; 93425 MW; CBF6983749B1FC15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
(Rel. 41, Last sequence update)
(Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 ARGDFPQAAQQLWLALQALGRPLPTSN 341
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ARGDFAQAAQQLWLALRALGRPLPTSH 27
                                                                                                                                                                                                                                                              PROSITE; PS50888; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                            24; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Similarity
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SREI MOUSE
ID SREI MOUSE
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DT 28-FEB-2003 (
DT 05-JUL-2004 (
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TISSUE SPECIFICITY: Isoform SREBP-1C predominates in liver,
adrenal gland, brain and adipose tissue, whereas isoform SREBP-1A
predominates in splean. Both isoforms are found in kidney, thymus,
testis, muscle, jejunum, and ileum.
PTM: Under sterol-depleted conditions, SREBPs are cleaved
sequentially by site-1 and site-2 protease. The first cleavage
occurs within the luminal loop and is directly regulated by
sterols. The second cleavage by site-2 protease occurs within the
first transmembrane stretch and liberates the soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription factor. Cleavage by the cysteine proteases, caspase-3 and caspase-7, is induced during apoptosis, independent of
                                                                                                                                                                                                                                                                                          SEQUENCE OF 42-444 FROM N.A. (ISOFORMS SREBP-1A-W42 AND SREBP-1C-W42) MEDLINE=99161303; Pubmed=10052151;
                                                                                                                                                                                                                                                                                                                              Inoue J., Sato R.;
"A novel splicing isoform of mouse sterol regulatory element-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sterol levels.

MISCELIAMBOUS: SREBPs have to be in a complex with the cleavage-activating protein (SCAP) to move to the Golgi and be cleaved by site-1 protease.

SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                       Shimomura I., Shimano H., Horton J.D., Goldstein J.L., Brown M.S., "Differential expression of exons la and lc in mRNAs for sterol regulatory element binding protein-1 in human and mouse organs and cultured cells.",
                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
Sterol regulatory element binding protein-1 (SREBP-1) (Sterol regulatory element-binding transcription factor 1).

Name=Srebfil, Synonyme=Srebpl;
Mus musculus (Mouse).
                                                                                                                                       SEQUENCE OF 1-41 FROM N.A. (ISOFORMS SREBP-1A AND SREBP-1C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mouse Srebpl.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                 Biosci. Biotechnol. Biochem. 63:243-245(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=SREBP-1A-W42;
IsoId=Q9WTN3-2; Sequence=VSP_002152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=09WTN3-3; Sequence=VSP_002151;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 55-1134 FROM N.A.
Lloyd D.J., Shackleton S., Trembath R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9WTN3-1; Sequence=Displayed;
                                                                                                                                                                           MEDLINE=97216050; PubMed=9062340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=SREBP-1C-W42;
                                                                                                                                                                                                                                                                                                                                                               protein-1 (SREBP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=SREPB-1A;
                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                          rissue=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hulo C.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNEL outstarion the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSS0888; HLH; 1. Actions; Cholesterol metabolism; DNA-binding; Activator; Alternative splicing; Cholesterol metabolism; Nuclear protein; Endoplasmic reticulum; Golgi stack; Lipid metabolism; Nuclear protein; Transcription regulation; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helix-loop-helix motif (By similarity).
Leucine-zipper (Potential).
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Cleavage (by S1P) (By similarity).
MDELAFGEAALEQITAEMCELDTAVINDI -> MDCTF
(in isoform SREBP-IC and isoform SREBP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage (by caspase-3 and caspase-7) similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (In isoform SREBP-1A-W42 and isoform SREBP-1C-W42).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential).
TRANSCRIPTIONAL ACTIVATION (ACIDIC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          510 S -> T (in Ref. 3).
613 P -> A (in Ref. 3).
621 L -> I (in Ref. 3).
625 S -> L (in Ref. 3).
633 C -> W (in Ref. 3).
634 H -> A (in Ref. 3).
7120505 MM, PEOF184F2A4PBTD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                           MGD; MGI:10504; -.bfl.
GO; GO:0005634; Cinucleus; IDA.
GO; GO:0003700; F:transcription factor activity; IDA.
GO; GO:004549; P:regulation of transcription; IDA.
InterPro; IPR001092; HLH—basic.
Pfam; PF00010; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential)
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2; Mismatches
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                                                                                                                                                            L) ALGOGOGE;
-; NOT ANNOTATED CDS.
L) AL132428;
-; NOT ANNOTATED CDS.
L) AA475250;
-; NOT ANNOTATED CDS.
L) A1386259;
-; NOT ANNOTATED CDS.
L) A1386259;
-; NOT ANNOTATED CDS.
L) A1552487;
-; NOT ANNOTATED CDS.
L) A1552781;
-; NOT ANNOTATED CDS.
L) A1597480;
-; NOT ANNOTATED CDS.
L) A7374266;
AAK54762.1;
-; AF374266;
AAK54762.1;
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                                                                                                                                               EMBL; AB017337; BAA74795.1; -
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24; Conservative
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1134 AA;
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EMBL; AF77426; AAK5
HSSP, P36956; IAM9
TRANSFAC; T04562; -
MGD; MGI:107606; Sre
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                                                                                                                 November 10, 2004, 11:41:17; Search time 8.93518 Seconds (without alignments) 222.664 Million cell updates/sec
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1: /cgn2_6/prodate/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodate/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodate/1/iaa/6A_COMB.pep:*
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6: /cgn2_6/prodate/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-382-911-4
US-08-382-911-6
US-09-382-911-6
US-09-382-911-6
US-09-412-545-2
US-09-240-236-2870
US-09-868-758-2
US-09-868-758-4
US-09-868-758-4
US-09-868-758-4
US-09-868-758-4
US-09-868-758-4
US-09-935-038A-2
US-09-782-165-97
US-09-783-185-2187
US-09-783-185-2187
US-09-646-67-93-61
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164
1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30
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                                                                                                                                                                                                                                                                                                                                          478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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61, Appl
4, Appl
44, Appl
4406, Ap
4406, Ap
47, Appl
47, Appl
23, Appl
23, Appl
260, Ap
260, Ap
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260, Appl
86, Appl
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86, Appl
86, Appl
86, Appl
88, Appl
                                      Sequence Seq
                                                                 US-09-198-452A-441
US-09-543-6BA-4406
US-08-553-6BA-4406
US-08-834-306-47
US-08-933-674A-47
US-09-938-110-5260
US-09-583-110-5260
US-09-684-708A-23
US-09-643-6B1A-7404
US-09-543-6B1A-7404
US-09-543-6B1A-7404
US-09-543-6B1A-7404
US-08-652-877-84
US-08-652-877-86
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ALIGNMENTS

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yesuence 4, Application US/09382911

Patent No. 622168

GENERAL INFORMATION:
APPLICANT: Prescott, Steven M.
APPLICANT: Bunting, Michaeline
APPLICANT: Topham, Matthew
TITLE OF INVENTION: Diacylglycerol Kinase Isoforms Epsilon and Zeta and
TITLE OF INVENTION: Methods of Use Thereof
TITLE OF INVENTION: Methods of Use Thereof
TITLE OF PLACATION NUMBER: US/09/382,911
CURRENT APPLICATION NUMBER: US/09/382,911
CURRENT FILING DATE: 1999-06-25
PRIOR FILING DATE: 1997-04-22

PRIOR FILING DATE: 1997-04-22

PRIOR APPLICATION NUMBER: 60/016,210
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                                                                     Sequence 4, Application US/08841483B
; Sequence 4, Application US/08841483B
; Patent No. 5976875
; GENERAL INFORMATION;
; APPLICANT: Bunting, Michaeline
; APPLICANT: Bunting, Michaeline
; APPLICANT: Tang, Wen
; APPLICANT: Tang, Wen
; TITLE OF INVENTION: Diacylglycerol Kinase Isoforms Epsilon and Zeta and
; TITLE OF INVENTION: Methods of Use Thereof
; TITLE OF INVENTION: MAPBER: US/08/841,483B
; CURRENT FILING DATE: 1997-04-22
; EARLIER FILING DATE: 1996-04-22
; NUMBER OP SEQ ID NOS: 33
; SOPTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 928
; MAPPLICATION OFF. DATE
; MAPPLICATION WENDER: MAPPLICATION
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92.7%; Score 152; DB 2; Length 92

Best Local Similarity 93.3%; Pred. No. 1.6e-14;

Matches 28; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
RESULT 1
US-08-841-483-4
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US-09-382-911-4
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; ORGANISM: M.catarrhalis
US-09-540-236-2870
  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-911-6
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ORGANISM: Homo sapiens
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US-09-248-796A-15653
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Patent No. 6221658
GENERAL INFORMATION:
APPLICANT: Prescott, Steven M.
APPLICANT: Tang, Wen
APPLICANT: Tang, Wen
APPLICANT: Tophan, Matthew
ITILE OF INVENTION: Diacylglycerol Kinase Isoforms Epsilon and Zeta and
ITILE OF INVENTION: Methods of Use Thereof
ITILE OF INVENTION: Methods of Use Thereof
ITILE OF INVENTION WHERE: US/09/382,911
CURRENT FILING DATE: 1999-08-25
FRICH APPLICATION NUMBER: 08/41,483
PRICH APPLICATION NUMBER: 60/016,210
PRICH APPLICATION NUMBER: 60/016,210
PRICH REPUBLICATION NUMBER: 60/016,210
PRICH PRILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.0
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Patent No. 5976875

GENERAL INFORMATION:
APPLICANT: Prescott, Steven M.
APPLICANT: Bunting, Michaeline
APPLICANT: Topham, Matthew
TITLE OF INVENTION: Diacylglycerol Kinase Isoforms Epsilon and Zeta and
TITLE OF INVENTION: Diacylglycerol Kinase Isoforms Epsilon and Zeta and
TITLE OF INVENTION: Matthew
TITLE OF INVENTION: MATHER: 1997-04-22

CURRENT FILING DATE: 1997-04-22

CURRENT FILING DATE: 1996-04-22

MUMBER: OF SEQ ID NOS: 33

NUMBER: PATENTING DATE: 1996-04-22

NUMBER: PATENTING DATE: 1996-04-22

NUMBER: PATENTING DATE: 1996-04-22

SEQ ID NOS: 33

SOFTWARE: PATENTING VET: 2.0

SEQ ID NOS: 33
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                                                                                                                                                                                                   Query Match
92.7%; Score 152; DB 3;
Best Local Similarity 93.3%; Pred. No. 1.6e-14;
Matches 28; Conservative 1; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                         495 GSSKDLAKHIRVVCDGMDLTPKIQDLKPQC 524
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PRIOR FILING DATE: 1996-04-22
                   NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 928
                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-911-4
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ORGANISM: Homo sapiens
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SEQ ID NO 6
LENGTH: 1117
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US-08-841-483-6
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Sequence 280.0, Application US/09540236

Batent No. 6673910
GENERAL INFORMATION:
APPLICANT GARY L.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NOS: 3840
LENGTH: 409
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Query Match 92.7%; Score 152; DB 3; Length 1117; Best Local Similarity 93.3%; Pred. No. 2e-14; Matches 28; Conservative 1; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Patent No. 6255095

Jednert No. 6255095

Jednert No. 6255095

Jednert No. 6255095

Jednert Persont, Stephen M.

APPLICANT: Presont, Stephen M.

APPLICANT: Traer, Elie

JITLE OF INVENTION: HUMAN DIACYLGLYCEROL KINASE IOTA

FILE REPERSENCE: 1321.2.25

CURRENT APPLICATION NUMBER: US/09/412,545

CURRENT FILING DATE: 1999-10-05

EARLIER APPLICATION NUMBER: 60/103,079

EARLIER PILING DATE: 1999-10-05

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0

LENGTH 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.0%; Score 118; DB 3; L
Best Local Similarity 72.4%; Pred. No. 2.9e-09;
Matches 21; Conservative 5; Mismatches 3;
                                                                                                                                           684 GSSKDLAKHIRVVCDGMDLTPKIQDLKPQC 713
                                                                                                           1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30
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Best Local Similarity 32.1%; Pred. No. 1.5;
Matches 9; Conservative 8; Mismatches 11; Indels
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US-09-868-758-2

Sequence 2, Application US/09868758

PAPLICANT: G12AXO Wellcome KK

APPLICANT: Takemocto, Yoshihiro

APPLICANT: Takemocto, Yoshihiro

APPLICANT: Hashimocto, Yasuhiro

TITLE OF INVERION: IKK3

FILE REFERENCE: 9950986P

CURRENT APPLICATION NUMBER: US/09/868,758

CURRENT APPLICATION NUMBER: GB 9828704.8

PRIOR FILING DATE: 1998-12-24

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 2

LENGTRARE: Patentin Ver. 2.1

SEQ ID NO 2
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APPLICAMY: Claxo Wellcome KK; APPLICAMY: Takemoto, Yoshihiro; APPLICAMY: Hashimoto, Yashihiro; APPLICAMY: Hashimoto, Yashihiro; TILLE REFERENCE: 99509669; CURRENT APPLICATION NUMBER: US/09/868,758; CURRENT FILING DATE: 1998-12-24; NUMBER: OF SEQ ID NOS: 45; SOFTWARR: PatentIn Ver: 2.1; SEQ ID NO 41
LENGTH: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.5%; Score 50; DB 56.2%; Pred. No. 40; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                       13 ANKDVDKQVQALIDEIDRNPNLTDKEKQ 40
                                                                                                                                                                                                                                                                                           2 SSKDLAKHIQVVCDGMDLTPKIHDLKPQ 29
                                  527:
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ORGANISM: Artificial Sequence
FEATURE:
                           INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
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Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-09-868-758-2
                                                                                                                                                                         US-08-936-165A-527
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US-09-868-758-41
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Sequence 15653, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15653
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TITLE OF INVENTION: No. 6348582el Prokaryctic Polymucleotides,
TITLE OF INVENTION: Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STREET: 709 Swedeland Road
CITY: King of Prussia
STREET: 19406-0939
COMPUTER: BA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: PASSEE OF Windows Version 2.0
COMPUTER: PASSEE OF Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Each and R
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 KHIQVVCDGMDLTPKIHDLK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Knowles, David
Lonetto, Michael
Lonetto, Richard
Pratt, Julie
Reichard, Richard
Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Black, Michael
Burnham, Martin
Hodgson, John
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-15653
                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 50.0 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-936-165A-527
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Gaps

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Query Match 30.5%; Score 50; DB 4; Length 716; Best Local Similarity 56.2%; Pred. No. 40; Matches 9; Conservative 3; Mismatches 4; Indels
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Best Local Similarity
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; OTHER INFORMATION: Description of Artificial Sequence: DT7-IKK3; OTHER INFORMATION: mutant US-09-868-758-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: DT7-IXK3 OTHER INFORMATION: mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: DT7-IKK3 // OTHER INFORMATION: mutant US-09-868-758-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 30.5%; Score 50; DB 4; Length 716; Similarity 56.2%; Pred. No. 40; 9; Conservative 3; Mismatches 4; Indels
                                                                                 DB 4; Length 716; 40;
                                                                                                                              4; Indels
                                                                                 30.5%; Score 50; DB
ilarity 56.2%; Pred. No. 40;
Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                GAUGHEAL INCORNATION:
APPLICANT: Glaxo Wellcome KK
APPLICANT: Tarkemctor, Yoshihiro
APPLICANT: Tarkemctor, Yoshihiro
APPLICANT: Tarkemctor, Yasuhiro
TITLE OF INVENTION: IKX3
FILE REFERRNCE: 9950966P
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: GB 9828704.8
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 42
LENGTH: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43, Application US/09868758
Patent No. 6576439
GENERAL INFORMATION:
APPLICANT: Glaxo Wellcome KK
APPLICANT: Takemoto, Yoshihiro
APPLICANT: Takemoto, Yoshihiro
APPLICANT: Bakai, Yutaka
APPLICANT: Hashimoto, Yasuhiro
TILLE OF INVENTION: IKK3
FILE REFERENCE: 9950986P
CURRENT APPLICATION NUMBER: US/09/868,758
CURRENT FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 45
SSOFTMARE: PatentIn Ver. 2.1
SSOFTMARE: PatentIn Ver. 2.1
SSOFTMARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                       RESULT 11
US-09-868-758-42
Sequence 42, Application US/09868758
Patent No. 6576439
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677 KDLLLHMQELCEGMKL 692
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677 KDLLLHMQELCEGMKL 692
                                                                                                                                                                 4 KDLAKHIQVVCDGMDL 19
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                    Query Match
Best Local Similarity
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Best Local Similarity
Matches 9; Conserve
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US-09-868-758-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: DT7-IKK3; OTHER INFORMATION: mutant
US-09-868-758-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.5%; Score 50; DB 4; Length 716; Best Local Similarity 56.2%; Pred. No. 40; Matches 9; Conservative 3; Mismatches 4; Indels
                                                                                                                 US-09-868-758-44

Sequence 44, Application US/09869758

PRECED NO. 6576439

GENERAL INFORMATION:
APPLICANT: Glaxo Wellcome KK
APPLICANT: Glaxo Wellcome KK
APPLICANT: Sakai, Yutaka
APPLICANT: Sakai, Yutaka
APPLICANT: Bashimoto, Yasuhiro
TITLE OF INVENTION: IKK3
FILE REFERENCE: 9950986P
CURRENT APPLICATION NUMBER: US/09/868,758
CURRENT APPLICATION NUMBER: GB 9828704.8

PRIOR FILING DATE: 1998-12-24
NUMBER: OF SEQ ID NOS: 45

SEQ ID NO 44
LENGTH: 716

LENGTH: 716

TOWER: DEFE
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j FALERAL INCORNATION:
APPLICANT: Glaxo Wellcome KK
APPLICANT: Takemcto, Yoshihiro
APPLICANT: Takemcto, Yoshihiro
APPLICANT: Bakin, Yutashiro
TITLE OF INVENTION: IKK3
FILE REFERENCE: 9950986P
CURRENT APPLICATION NUMBER: US/09/868,758
CURRENT FILING DATE: 2001-09-27
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SENGTHA: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-868-758-45; Sequence 45, Application US/09868758; Patent No. 6576439
                          ||| |:|:|| |
677 KDLLLHMQELCEGMKL 692
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677 KDLLLHMQBLCEGMKL 692
4 KDLAKHIQVVCDGMDL 19
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                               RESULT 15
US-09-935-038A-2
is Sequence 2, Application US/09935038A
j Patent No. 6743603
j GENERAL INFORMATION:
j APPLICANT: Wock, Simon
j APPLICANT: Wock, Simon
j APPLICANT: Male Healthcare Network
j TITLE OF INVENTION: No. 6743603e1 Tumor Suppressor Encoding Nucleic
j TITLE OF INVENTION: No. 6743603e1 Tumor Suppressor Encoding Nucleic
j TITLE OF INVENTION: No. 6743603e1 Tumor Suppressor Encoding Nucleic
j TITLE OF INVENTION: No. 6743603e1 Tumor Suppressor Encoding Nucleic
j TITLE OF INVENTION: 2010-08-22
j CURRENT APPLICATION NUMBER: US/09/935, 038A
j PRIOR FILING DATE: 2000-08-22
j PRIOR FILING DATE: 2000-08-22
j PRIOR FILING DATE: 2000-08-22
j ROWGRAN FILING DATE: 2000-08-22
j ROWGRAN: FastSEQ for Windows Version 3.0
j SEQ ID NO 2
j LENGTH: 377
j TYPE: PRT
j ORGANISM: Homo sapiens
US-09-935-038A-2
     Gaps
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     4; Indels
  3; Mismatches
                                                                               677 KDLLLHMQELCEGMKL 692
                                             4 KDLAKHIQVVCDGMDL 19
9; Conservative
  Matches
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Search completed: November 10, 2004, 12:32:34 Job time : 9.93518 secs

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November 10, 2004, 15:53:52; Search time 28.9352 Seconds (without alignments) 366.225 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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164
1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30
                                                                                             OM protein - protein search, using sw model
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

1566620 seqs, 353225886 residues

Gapop 10.0 , Gapext 0.5

Perfect score:

Title:

Run on:

Sequence:

Scoring table:

Searched:

Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/PcT_PubCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PcT_Par_Pub.pep:*

3: \cgn2_6/ptodata/1/pubpaa/PcT_Par_Pub.pep:*

4: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

9: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

14: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

15: \cgn2_6/ptodata/1/pubpaa/USO0PUBCOMB.pep:*

16: \cgn2_6/ptodata/1/pubpaa/USOD_PUBCOMB.pep:*

17: \cgn2_6/ptodata/1/pubpaa/USOD_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/USOD_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USOD_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USOD_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USOD_PUBCOMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Sci	Score	Query Match	Query Match Length DB	DB	ID	Description
	164	100.0	30	14	US-10-092-750-23	Sequence 23, Appl
^1	152	92.7		σ	US-09-764-868-1054	Sequence 1054, Ap
_	152	92.7		14	US-10-170-385-353	Segmence 353, App
	152	92.7		14	US-10-205-194-7	Sequence 7, Appli
ın	118	72.0		σ	US-09-771-161A-239	Sequence 239, App
	118	72.0		16	US-10-408-765A-582	Sequence 582, App
7 5	7.5	35.1	9	17	US-10-425-115-294496	Sequence 294496,
~	54	32.9		16	US-10-437-963-156582	Sequence 156582,
9	0.5	30.8		15	US-10-229-345-3	Sequence 3, Appli
	0.5	30.8		15	US-10-274-177-3	Sequence 3, Appli
เก	0.5	30.8		16	US-10-650-112-3	Sequence 3, Appli
N.	0.5	30.8		14	US-10-295-027-124	Sequence 124, App
Ñ	0.5	30.8		14	US-10-295-027-1186	Sequence 1186, Ap

Appl	Appl	Appl	Appl	ildak	App	4, App	App	App	7, Ap	Appl	Appl	App	Appl	App	App	Appl	Appl	81,	App	ilda	Appli	Appl	Appl	Appl	Appl	Appl	Appl	Ap	7, A	A.	1, A
87,	14,	14,	14.	2,	122,	764,	777	883,	1187		85,		•	27,		30,				2, 4			42,					83	7017	66	4381
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173-5	229-3	274-1	S	30-	σ	295-0	5	295-0	5	087-0	3-		173-9	39-98	279-0	219-6	219-8	7	369-4	O.	408-6	108-6	9-801	108-6	9-801	408-6	394-3	15-24	82-1	15-24	82-1
-10-	-10-	-10-	-10-	-60	-10-	10-	-10-	10-	-10-	6	-10-	-10	-10	-09-93	-10-2	-10-	-110-	-10-	-10-	6	-10	-10-4	10	-10	-10-4	-10-4	-10-	39-81	-10-	09-83	-10-
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ALIGNMENTS

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Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 30; Conservative 0; Mismatches 0; Indels
              Sequence 22, Application US/10092750
Sequence 22, Application US/10092750
Publication No. US20030032157A1
GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia
APPLICANT: Might, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REPRENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2002-03-07
FRIOR APPLICATION NUMBER: US 60/274,526
FRIOR APPLICATION NUMBER: 203-03-07
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-10-092-750-23
US-10-092-750-23
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1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30 RESULT 2
US-09-764-868-1054
Sequence 1054, Application US/09764868
Parent No. US20020168711A1
GENERAL INFORMATION: g

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Homo sapiens
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Best Local Similarity
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US-09-771-161A-239
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LENGTH: 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
LOCATION: (50)
LOCATION: (50)
LOCATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (331)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . LOCATION: (545); CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-868-1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERBUTED: PLOZ3
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1054
LENGTH: S84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

92.7%; Score 152; DB 14; Length 928;
Best Local Similarity 93.3%; Pred. No. 1.2e-13;
Matches 28; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 92.7%; Score 152; DB 9; Length 584; Best Local Similarity 93.3%; Pred. No. 7e-14; Matches 28; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 GSSKDLAKHIRVVCDGMDLTPKIQDLKPQC 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BILLEY, KALIE MATY
APPLICANT: RAYDEY, KALIE MATY
APPLICANT: RAYDEY, William Nigel
APPLICANT: Naylor, Stuart
APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
TITLE OF INVENTION: ANALYSIS METHOD
TITLE OF INVENTION: ANALYSIS METHOD
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: PESESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 353
LENGTH: 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ward, Neil Raymond
APPLICANT: Mundy, Christopher Robert
APPLICANT: Kan, On
APPLICANT: Harris, Robert Alan
APPLICANT: White, Jonathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 353, Application US/10170385 Publication No. US20030203372A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-353
                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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495 GSSKDLAKHIRVVCDGMDLTPKIQDLKPQC 524

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                                                                                                     APPLICANT: Marie Long Alistair
APPLICANT: Dixon, Alistair
APPLICANT: Dixon, Alistair
APPLICANT: Brookbank, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REPERENCE: WL-A-018201
CURRENT APPLICATION NUMBER: US/10/205,194
CURRENT FILING DATE: 5200-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR PILING DATE: 2001-07-27
SOFTWARE: PATENTING DATE: 2010-07-27
SOFTWARE: PATENTING DATE: 2010-07-27
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1. Similarity 72.4%; Pred. No. 1.7e-08;
21; Conservativé 5; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 92.7%; Score 152; DB 14; Length 929; Best Local Similarity 93.3%; Pred. No. 1.2e-13; Matches 28; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INVENTATION: et al.

APPLICART: LEVINE, et al.

TILLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFRENCE: 802260-2005.1

FULE REPRENCE: 802260-2005.1

CURRENT APPLICATION NUMBER: U9/724,676

PRIOR APPLICATION NUMBER: 136776

PRIOR APPLICATION NUMBER: 136776

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 273

SOFTWARE: PATCHIN VARIEN: 13519

KED ID NO 239

LENGTH: 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: Diacylglycerol kinase US-10-205-194-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 582, Application US/10408765A; Publication No. US20040101874A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 239, Application US/09771161A Patent No. US20020110811A1 GENERAL INFORMATION:
Sequence 7, Application US/10205194 Publication No. US20030134301A1 GENERAL INFORMATION:
                                                                                    APPLICANT: Warner-Lambert Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-10-408-765A-582
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Gaps

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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 156582
LENGTH: 318
TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.8%; Score 50.5; DB 15; Length 732; Best Local Similarity 42.9%; Pred. No. 1.4e+02; Matches 9; Conservative 7; Mismatches 4; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.9%; Score 54; DB 16; Length 318; Best Local Similarity 43.5%; Pred. No. 16; Matches 10; Conservative 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-229-345-3
; Sequence 3, Application US/10229345
; Publication No. US20040038220A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; CURRENT PRILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10274177
; Publication No. US20040038255A1
; Publication No. US20040038255A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; TILE REFERENCE: CWRU-P01-003
; CURRENT APPLICATION NUMBER: US/10/274,177
; CURRENT PILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/10/229,345
; PRIOR APPLICATION NUMBER: US/10/229,345
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PATENTH VERSION 3.1
; SEQ ID NO 3
; LENGTH: 732
                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Clone ID: PAT_MRT4530_56235C.1.pep
US-10-437-963-156582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 ASRDLALDLQLVRNGLDRTSRFH 112
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ORGANISM: Homo sapiens
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COGANISM: Homo sapiens
US-10-274-177-3
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Best Local Similarity
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US-10-274-177-3
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| Publication No. US20040114272A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: La Royalf, David K.
| APPLICANT: Cao, Yongan T.
| APPLICANT: Cao, Yongan T.
| TITLE OF INVENTION: Plants
| UURRENT APPLICATION NUMBER: US/10/425,115
| CURRENT PLING DATE: 2003-04-28
| UNDER OF SEQ ID NOS: 369326
| SEQ ID NO 294496
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             APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Garno, Gary W.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION NUMBER: US/10/408,765A
CURRENT PILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5892
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35.1%; Score 57.5; DB 17; Length 60;
Best Local Similarity 52.4%; Pred. No. 0.7;
Matches 11; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: MRT4577_31667C.1.pep
US-10-425-115-294496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 576 SSRDLSKHVKVVCDGTDLTPKIQELKFQC 604
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 NLQLVCNGI-LTSKIHTLRPR 30
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  hosh, Soumitra S.
Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-582
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ORGANISM: Zea mays
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US-10-425-115-294496
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PUDLICATION NO. US2001022350A1
GENERAL INFORMATION:
APPLICANT Afai, Macasha
APPLICANT Ginsberg, Wendy M.
APPLICANT Ginsberg, Ward M.
APPLICANT Ginsberg, Ward M.
APPLICANT Gish, Kurt C.
APPLICANT Gish, Kurt C.
APPLICANT Hevel, Packer A.
APPLICANT Back Biotechnology, Inc.
APPLICANT Watson, Susan R.
APPLICANT: Watson, Watson, Watson, Sologe, Susan R.
FILE REFERENCE: 108504-012500US
CURRENT FILING DATE: 2000-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/332, 464
PRIOR PILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/340, 376
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2002-01-09
PRIOR PILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-01
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-03
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Publication No. US20030232350A1
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SEQ ID NO 1186
LENGTH: 755
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-124
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; ORGANISM: Homo sapiens
US-10-295-027-1186
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| Sequence 3, Application US/10650112
| Publication No. US20040110712A1
| GENERAL INFORMATION:
| APPLICANT NARKOWITZ, Sanford D.
| TITLE OF INVENTION: WETHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
| TITLE OF INVENTION: WETHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS
| CURRENT APPLICATION NUMBER: US/10/650,112
| CURRENT FILING DATE: 2003-08-26
| PRIOR FILING DATE: 2002-08-26
| PRIOR FILING DATE: 2002-08-27
| NUMBER OF SEQ ID NOS: 27
| SOFFWARE: Patentin version 3.2
| LENGTH: 732
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APPLICANT: Mateon, Susan R.
APPLICANT: Wateon, Susan R.
APPLICANT: Wateon, Susan R.
APPLICANT: Wateon, Susan R.
TITLE OF INVENTION: Methods of Diagnosis of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 01850-01250003
CURRENT APPLICATION NUMBER: US 108/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR PELLING DATE: 2000-09-15
PRIOR PELLING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PLING DATE: 2001-11-15
PRIOR PLING DATE: 2001-11-15
PRIOR PLING DATE: 2001-11-15
PRIOR PLING DATE: 2001-11-29
PRIOR PLING DATE: 2001-12-29
PRIOR PLING DATE: 2001-12-39
PRIOR PLING DATE: 2001-12-29
                 Gaps
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                 Indels
                 7; Mismatches
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Publication No. US20030232350A1
GENERAL INFORMATION:
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                                                                                    3 SKDLAKHIQV-VCDGMDLTPK 22
                                                                                                                                                43 SFERSKHFAITVCDGLDISPE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ::|| : ||||:|:||:|| SFERSKHFAITVCDGLDISPE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsh, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 42.9°
Matches 9; Conservative
                 9; Conservative
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US-10-650-112-3
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Sequence 87, Application US/10173999
; Bublication No. US20040005563A1
; GENERAL INPORMATION:
GENERAL INPORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Gish, Kurt C.
; TITLE OF INVENTION: and Methods of Diagnosis of Covarian CITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: and Methods of Screening for Modulators of CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT APPLICATION NUMBER: US 60/299,234
; PRIOR PAPLICATION NUMBER: US 60/299,234
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR PILING DATE: 2001-08-27
; PRIOR PILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR PILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO 87:
**LENGTH: 755
**THEORY OF SEQ ID NOS: 163
**THEORY OF 
                                                                                           1;
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Query Match 30.8%; Score 50.5; DB 14; Length 755; Best Local Similarity 42.9%; Pred. No. 1.5e+02; Matches 9; Conservative 7; Mismatches 4; Indels 1;
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30.8%; Score 50.5; DB 15; Length 755;
Best Local Similarity 42.9%; Pred. No. 1.5e+02;
Matches 9; Conservative 7; Mismatches 4; Indels 1.
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US-10-229-345-14
i Sequence 14, Application US/10229345
publication No. US20040038220A1
GENERAL INFORMATION:
APPLICANT: MARKOWITZ, Sanford D.
TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
FILE REFERENCE CWRU-PO1-003
CURRENT APPLICATION NUMBER: US/10/229,345
CURRENT PILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 755
                                                                                                                                                                 3 SKDLAKHIQV-VCDGMDLTPK 22
                                                                                                                                                                                                                 66 SFERSKHFAITVCDGLDISPE 86
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CRGANISM: Homo sapiens
US-10-173-999-87
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ORGANISM: Homo sapiens
US-10-229-345-14
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US-10-173-999-87
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66 SFERSKHFALTVCDGLDISPE 86
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Search completed: November 10, 2004, 16:36:07 Job time: 29.9352 secs

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Page

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GenCore version 5.1.6
Copyright (c) 1993.- 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 11:36:51; Search time 6.06481 Seconds (without alignments) 475.942 Million cell updates/sec

Run on:

Title:
US-10-092-750-23
Perfect score: 164
Sequence: 1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30

Sequence: 1 GSSKDLAKH1QVVCDGMDLTPK
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	diacylqlycerol kin		hypothetical prote	hypothetical prote	DNA gyrase-like pr	diacylglycerol kin	inositol-3-phospha	glucose-6-phosphat	mRNA capping enzym	hypothetical prote		_	끖	conserved hypothet	hypothetical prote	ซ	Neutrophil attract	regulatory compone	phosphoribosyl-AMP	integrase homolog	diacylglycerol kin	glycine-tRNA ligas	glycyl-tRNA synthe	ы	diacylglycerol kin	'n		-H	superoxide dismuta
SUMMAKIES	QI	JC6124	T34334	D70895	T15789	-	T13709	10		10	10	B89921	B86203	NRRT	F81689	F71534	C42594	I48148	S74986	YNECHI	A69774	\$28229	F71040	C75174	D84920	A46140	B46140	T33754	ΗĐ	JC5718
	. 80	01	N	N	N	a	Ŋ	N	7	N	~	N	~	н	n	N	Н	N	N	Н	~	7	~	~	~	N	N	N	Н	N
	Length	929	930	262	7829	818	1454	525	541	607	822	6713	<u>თ</u>	152	186	188	592	101	147	203	368	517	570	571	635	σv	796	ω	N	O)
•	% Query Match	92.7	Н	31.7	31.4	31.1	-	ö	ö	。	٥.	o.	ο.	ο.	29.9	o,	σ.	φ.	o,	ď.	ა.	ď.	ď	ο.	ο,	σ,	φ.	σ.	29.0	σ.
	Score	152	84	52	51.5	51	51	20	20	20	20	20	49	49	49	49	49	48	48	48	48	48	48	48	48	48	48	48	7.	•
	Result No.	1	2	m	4	Ŋ	9	7	ω	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

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Ouery Match 51.2%; Score 84; DB 2; Length 930; Best Local Similarity 51.7%; Pred. No. 0.001; Matches 15; Conservative 7; Mismatches 7; Indels

lipopolysaccharide probable lipopolys translation initia	glucose-6-phosphat changed division r hymothetical ging	hypothetical prote hypothetical prote	hypothetical proterref(2)P protein	pancreatic ribonuc pancreatic ribonuc	pancreatic ribonuc hypothetical prote conserved hypothet
AC0973 D41317 G60315	T44843 T38929	13,003 B86908 T33811	F82396 S33561	A4/U/U NRCM NRCMB	NRCMM S50547 A99226
000	1000	100	000	7	100
100 100 100 100	775	313 421	505 594	124	124 148 157
700	28.7.7.	28.2	28.4	28.0	28.0 28.0 28.0
47.5	. 4 4 4 C	46.5	46.5	4 4 4 0 0 0	4 4 4 0 0 0
330	1 C C C	9 8 6 7 6	8 6 6 6 6	2 4 4 2 4 4	4 4 4 6 4 3

ALIGNMENTS

RESULT 1 diacylglycerol kinase (EC 2.7.1.107) IV - rat diacylglycerol kinase (EC 2.7.1.107) IV - rat diacylglycerol kinase (EC 2.7.1.107) IV - rat C;Species: Rattus norvegicus (Norway rat) C;Date: IcApr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004 C;Accession: JG6124 R;Goto, K.; Kondo, H. Proc. Natl. Acad Sci. U.S.A. 93, 11196-11201, 1996 A;Title: A 104-KDa diacylglycerol kinase containing ankyrin-like repeats localizes in the A;Reference number: JG6124; MUID:97008156; PMID:8855332 A;Contents: Tissue Retina, Brain A;Accession: JG6124 A;Molecule type: mRNA A;Residues: 1-929 <ggt> A;Content: This enzyme is involved in intranuclear processes, It plays a role in the atte C;Comment: This enzyme is involved in intranuclear processes, It plays a role in the atte C;Keywords: AfP binding; brain; phosphotransferase, zinc finger</ggt>
Query Match Best Local Similarity 93.3%; Pred. No. 2.3e-13; Matches 28; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GSSKDLAKHIQVVCDGWDLTPKIHDLKPQC 30
 RESULT 2 T34334 hypothetical protein K06Al.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T34334 R;Fulton, L. submitted to the EMBL Data Library, July 1995 A;Description: The sequence of C. elegans cosmid K06Al.
 A,Accession: T4334 A,Accession: T4334 A,Accession: T4334 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DNA A,Residues: 1-930 <full. 173="" 1;="" 2="" 265="" 2;="" 2<="" 300="" 3;="" 484="" 537="" 587="" 684="" 796="" 840="" 897="" a,cross-references:="" a,experimental="" a,gene:="" a,genetics:="" a,map="" a;introns:="" bmbl:u23449;="" bristol="" c,genetics:="" cesp:k06a1.6="" clone="" gspdb:gn00020;="" k06a1="" n2;="" pidn:aac24300.1;="" position:="" source:="" strain="" td=""></full.>

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Gaps ٠. د

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diacylglycerol kinase (EC 2.7.1.107) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: T13709
R;Masai I.; Okazaki, A.; Hosoya, T.; Hotta, Y.
Proc. Natl. Acad. Sci. US.A. 90, 1157-11161, 1993
A;Title: Drosophila retinal degeneration A gene encodes an eye-specific diacylglycerol kin A;Title: Drosophila retinal degeneration A gene encodes an eye-specific diacylglycerol kin A;Title: Drosophila retinal degeneration A gene encodes an eye-specific diacylglycerol kin A;Title: Drosophila retinal degeneration A gene encodes an eye-specific diacylglycerol kin A;Title: Drosophila retinal degeneration A gene encodes an eye-specific diacylglycerol kin A;Title: Drosophila retinal degeneration A gene in May A;Title: Mulpinary, translated from GB/EMBL/DDBJ
A;Genetics:
C;Genetics:
A;Conserics:
A;Conserics:
A;Conserics: FlyBase:FBgn0003217
C;Keywords: phosphotransferase
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T35872
S;Oliver, K; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
S;Oliver, K; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
S;Oliver, K; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
S;Oliver, K; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
S;Ocession: T35872
S;Accession: T35872
S;Coserreferences: UNIPROT:OSO510; EMBL:AL009204; PIDN:CAA15793.1; GSPDB:GN00070; SCOEDE
S;Experimental source: strain A3(2)
C;Genetics: SCOEDE:SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOEDE.SCOED
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R;Ainscough, R.
Submitted to the EMBL Data Library, December 1998
A;Reference number: 218979
A;Accession: T1856
A;Status: prediminary; translated from GB/EMBL/DDBJ
A;Reference undary; translated from GB/EMBL/DDBJ
A;Residues: 1-525 <WIL>
A;Residues: 1-525 <WIL>
A;Cross-references: UNIPROT:Q18664; EMBL:AL033535; PIDN:CAA22132.1; CESP:VF13D12L.1
B;Gajadsty, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.1%; Score 51; DB 2; Best Local Similarity 50.0%; Pred. No. 43; Matches 13; Conservative 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 KDLVGAKKIQGIADVKDLTDRAHGLR 314
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A;Molecule type: DNA
A;Residues: 1-262 <COL>
A;Cross-references: UNIPROT:053434; GB:AL021897; GB:AL123456; NID:g3256022; PIDN:CAA1720
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-7829 <BEN>
A;Cross-references: UNIPROT:Q18559; EMBL:U41541; NID:g1109867; PID:g1109869; PIDN:AAA831
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A; John Common 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mycobacterium tuberculosis
C;Stecies: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70895 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70895 # Sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
R;Connor, R:; Bavies, R:; Parkhill, J:; Gannier, T:; Churcher, C:; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J:; Rutter, S:; Seeger, K.; Skelton, S:; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R:; Sulston, J.E.; Taylor, K.; Whitehead, S:; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230
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C.Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Rv1086 - Mycobacterium tuberculosis (strain H37RV)
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31.7%; Score 52; DB 2; Length 262;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 9; Conservative 2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: Rv1086
C;Superfamily: conserved hypothetical protein YBR002c
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4730 SAKSLQKYVQVLCEFISNSAKSLHDI 4755
                                                                                       2 SSKDLAKHIQVVCDGMDLTPKIHDLKPQC
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Cispecies: Caenorhabditis elegans
Cibate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cibate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cibate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cibate: programmer of C. elegans cosmid T07F8.
Algebrance number: Z20102
Algebrance number: Z2
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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accesion: B8921
R;Kuroda, M.; Ohte, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; F.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
Lancet 357, 1225-1240, 2001
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Cross_references: UNIPROT:099U54; GB:BA000018; PID:gl3701232; PIDN:BAB42527.1; GSPDB:GR
A;Experimental source: strain N315
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 822;
59;
                                                  Length 607;
                                                                                                                       Indels
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B86203
hypothetical protein [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T07F8.1 - Caenorhabditis elegans
                                                  7
                                                                                    d. No. 43;
Mismatches
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                                              Score 50;
Pred. No. 4
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                                                                                                                                                                                                                                                              139 KDGIKHVKIAČRGRDAVP 156
                                                                                                                                                                                            27
                                              30.5%;
ilarity 44.4%;
Conservative
                                                                                                                                                                                            4 KDLAKHIQVVCDGMDLTP
                                              Query Match
Best Local Similarity
Matches 8; Conserva
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Matches 9; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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A;Gene: CESP:T07F8.1
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A; Introns: 678/3
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T25866
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(75358
glucose-6-phosphate isomerase - Deinococcus radiodurans (strain R1)
(5/Species: Deinococcus radiodurans
C/Species: Deinococcus radiodurans
C/Spacesion: C/SSSS
R/Species: Deinococcus radiodurans R.J.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/REference number: A/SSSO, MUID:20036896; PMID:10567266
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"RNA capping enzyme-like protein - Arabidopsis thaliana

"Alternate names: protein F703.270

"Alternate names: protein F703.270

"Alternate names: protein F703.270

"Alternate number: 2010 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T45569

R;Bevan, M; Zimmermann, W; Grueneisen, A; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lensubmitted to the Protein Sequence Database, January 2000
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A;Introns: 33/3; 73/1; 112/3; 146/3; 167/3; 212/3; 281/3; 321/3; 351/3; 398/3; 434/3; 46
A;Note: P7J8.270
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A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosedues: 1-525 <W12>
A;Cross-references: EMBL:Z69902; PIDN:CAA93771.1; GSPDB:GN00020; CESP:VF13D12L.1
A;Experimental source: clone C47D12
A;Genetics: A;Gene: CESP:VF13D12L.1
A;Map position: 2
A;Antrons: 106/2, 287/1; 411/2
C;Superfamily: myo-inositol-1-phosphate synthase
C;Keywords: intramolecular lyase; isomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 525;
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A;Experimental source: cultivar Columbia; BAC clone F7J8
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2
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A,Map position: 1
C,Superfamily: glucose-6-phosphate isomerase
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37 HFEHRADGLHVTPKEHDYSFKTVLKPR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                           30.5%;
Best Local Similarity 40.7%;
Matches 11; Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain R1
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-541 < WHI>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-607 <BEV>
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Best Local S
Matches 11
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Best Local Similarity 47.4
Matches 9; Conservative
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A,Molecule type: DNA
A,Residues: 1-186 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary Molecule type: DNA
                                                                                                                                                                                                C;Species: Chlamydia
C;Date: 31-Mar-2000 #
C;Accesion: F81689
R;Redd, T.D.; Brunhar
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: F81689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                           RESULT
F81689
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               Cidence: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
Cidencession: B86203
Cidencession: B86203
Cidence_revision 02-Mar-2001 #text_change 09-Jul-2004
Cidencession: B86203
Chin, C.W.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C. C.A.; Li, S., Li, Scham, R.; Suuhwick, A.W.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatic ribonuclease (EC 3.1.27.5) precursor - rat
N;Alternate names: RNase 1; RNase A
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A92356; A90585; A91313; A00831
R;MacDonald, R.U.; Stary, S.U.; Swift, G.H.
R;MacDonald, R.U.; Stary, S.U.; Swift, G.H.
A;Title: Rat pancreatic ribonuclease messenger RNA. The nucleotide sequence of the entix A;Reference number: A92356; MUD:83082740; PMID:7174650
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-99 <STO>
A;Cross-references: UNIPROT:Q9M9Y9; GB:AE005172; NID:g7523711; PIDN:AAF63150.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title: Rat pancreatic ribonuclease: agreement between the corrected amino acid sequend Reference number: A91313; MUID:83262417; PMID:6873294
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,Residues: 26-97,'D',99-123,'T',125,'N',127-128,'N',130,'E',132-152 <BBI>
,Beintema, U.J.
5BS Lett. 159, 191-195, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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C;Keywords: hydrolase; nucleic acid digestion; pancreas
E;1-25/Domain: signal sequence #status predicted <SIG>
F;26-152/Product: pancreatic ribonuclease #status experimental <MAT>
F;40,69.147/Accive site: His, Lys, His #status predicted
F;54-112,68-123,86-138,93-100/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beintema, J.J.; Gruber, M.
.ochim. Biophys. Acta 310, 161-173, 1973
Title: Rat pancreatic ribonuclease. II. Amino acid sequence.
Reference number: A90585; MUID:73194545; PMID:4710592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 2; Length 99;
Pred. No. 9.4;
6; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: glutaredoxin; glutaredoxin homology
C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: mRNA
Residues: 1-152 <MAC>
Cross-references: UNIPROT:P00684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 38.7%;
Matches 12; Conservative
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Thes 13; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                    Accession: B86203
Status: preliminary
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-----DLAKHIQVVCDGMDLTPKIH 24

1 GSSK---

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A,Cross-references: UNIPROT:Q9PKCl; GB:AB002323; GB:AB002160; NID:g7190585; PIDN:AAF39388; A;Experimental source: strain Nigg (MoPn)
C,Genetics:
A,Gene: TC0545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: Genome segrence of an obligate intracellular pathogen of humans: Chlamydia track A,Reference number: A71570; MUID:99000809; PMID:9784136
A,Accession: F71534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:084275; GB:AE001300; GB:AE001273; NID:g3328682; PIDN:AAC67866
A;Experimental source: serotype D, strain UM-3/Cx
                                                                                                                                                                                                                                                                          R,Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodeon, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Mccleic Acids Rees. 28, 1397-1466, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MJID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein CT273 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Ju1-2004
C;Accession: F71534
R;Srepheng, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
                                                                                                                                                             conserved hypothetical protein TC0545 [imported] - Chlamydia muridarum (strain Nigg) C,Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C,Date: 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Η;
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Pred. No. 18;
5; Mismatches 1
116 GSSKYPNCDYTTTDSQKHIIACDGNPYVP-VH 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49; DB 2;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
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Best Local Similarity 47.2.
Best Local Similarity 67.2.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 11:27:01; Search time 32.8241 Seconds (without alignments) 525.871 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-092-750-23 164 1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 1825181 seqs, 575374646 residues Searched:

1825181

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q91ys0 mus musculu	Q80up3 mus musculu	attr	Ollo	ОШО	ğ	ğ	homo	homo	Q810c4 rattus norv									Q910b9 streptomyce	neuros	oryza sa	Aas01975 oryza sat	Q9wux3 rattus ratt	_	7	9d0r	_	Q8egx4 shewanella	Q7vmul haemophilus	rke1	Aas93767 drosophil
	DI		KDGZ MOUSE	KDGZ RAT	Q62T25	Q6ZVG7	BAC85894	BAC86770	KDGZ HUMAN	QHIVW9	Q810C4	Q810C5	KDGI HUMAN	KDGM_CAREL	Q7QFJ1	Q7PCP4	Q8E8F9	QBEKM6	OBWOFO	Q9L0B9	Q7S6Y2	Q751P7		RNP_RATRT	Q8P644	Q9D5B7	ZFPP MYCBO	ZFPP MYCTU	Q8EGX4	Q7VMU1	Q9NKE1	AAS93767
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	Score	LO.	S	ŝ	152	S	S	2	L)	4	Н	Н	\vdash	84	65	62	58.5	56	54	54	23	23	23	52.5	ä	52	52	52	52	52	52	52
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Q832D4 Q18559 Q823N7 Q782N1 Q77E58 Q81CG3 O50510 Q7Q1B4 Q7VJ11 KDGE DROME Q8SY47 AASO5020	
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858 8
67 260 2
372 3
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DOMAIN
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SEQUENCE
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KDGZ RAT
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REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENTED TISSUB=Breast tumor;

RA SECURIS R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hischul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heisch B.

RA Stapleton M., Soarse M.B., Bonaldo M.F., Carninci P., Prange C.

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McGwan P.J., McKernan K.J., Mahk V.J., Mallahy S.J.,

RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RY Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

C. -- FUNCTION: Displaye a strong preference for 1,2-diacylglycerols over 1,3-diacylglycerols (By similarity).

C. -- CATALATIC ACTIVITY: ARP + 1,2-diacylglycerol = ADP + 1,2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                           10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Diacylglycerol kinase, zeta (EC 2.7.1.107) (Diglyceride kinase) (DGKzeta) (DAG kinase zeta).
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diacylglycerol 3-phosphate.
SUBUNIT: Interacts with the PDZ domain of the syntrophin SNTG1
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Wus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 2 ANK repeats.
-!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the eukaryotic diacylglycerol kinase
                                                                                                                                                  ö
                                                                                                                Query Match 92.7%; Score 152; DB 2; Length 458; Best Local Similarity 93.3%; Pred. No. 3.5e-13; Matches 28; Conservative 1; Mismatches 1; Indels
                                                                                   458 AA; 51141 MW; B68D9B2B9D9B9956 CRC64;
                                                                                                                                                                                                                                                                                              929 AA
                                                                                                                                                                                 1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30
                                                                                                                                                                                                  24 GSSKDLAKHIRVVCDGMDLTPKIQDLKPQC 53
SMART; SM00045; DAGKa; 1.
PROSITE; PS50088; ANK_REPEAT; 2.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                    ANK repeat.
                                                                                                                                                                                                                                                                                              MOUSE
                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family
                                                                                                                                                                                                                                                                                                                                                                                                             Name=Dqkz
                                                                                                                                                                                                                                                              RESULT 2
KDGZ_MOUSE
ID KDGZ_MOU
AC Q80UF3;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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"A 104-kDa disaylglycerol kinase containing ankyrin-like repeats
"A 104-kDa disaylglycerol kinase containing ankyrin-like repeats
localizes in the cell nucleus.";

Proc. Natl. Acad. Sci. U.S.A. 93:11196-11201(1996).

-!- FUNCTION: Displays a strong preference for 1,2-diacylglycerols
over 1,3-diacylglycerols, but lacks substrate specificity among
molecular species of long chain diacylglycerols.

-!- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-
diacylglycerol 3-phosphate.
-!- SUBMNT: Interacts with the PDZ domain of the syntrophin SNTG1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Diacyllglycerol kinase, zeta (EC 2,7.1.107) (Diglyceride kinase)
zeta) (DAG kinase zeta) (DGK-IV) (104 kba diacylglycerol kinase)
Name-DGkz; Synonyms-Dagké;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 152; DB 1; Length 929;
Pred. No. 7.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phorbol-ester and DAG binding
Phorbol-ester and DAG binding
                                                                                                         InterPro; IRRO0110; ANK.
InterPro; IRRO01210; DAGKa.
InterPro; IRRO01206; DAGKa.
InterPro; IRRO01206; DAGKa.
InterPro; IRRO01206; DAGKa.
InterPro; IRRO01209; DAG PE-bind.
InterPro; IRRO01219; DAG PE-bind.
InterPro; IRRO01219; DAGK act; I.
InterPro IRRO119; DAGK act; I.
InterPro IRRO119; DAGK act; I.
InterPro IRRO119; DAGKa; I.
IRRO119; PRO019; DAGKa; I.
IRRO119; PRO019; DAGKa; I.
IRRO119; PRO019; DAG PE BIND DOM 1; FALSE NEG.
IRRO119; PRO019; DAG PE BIND DOM 2; FALSE NEG.
IRRO119; PRO019; DAG PE BIND DOM 2; FALSE NEG.
IRRO119; PRO019; DAG PE BIND DOM 2; FALSE NEG.
IRRO119; DAG PE BIND DOM 2; FALSE NEG.
IRRO119; DAG PE BIND DOM 2; PALSE NEG.
IRRO119; DAG PE BIND DOM 3; PALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catalytic-A (Potential).
Catalytic-B (Potential).
ANK 1.
ANK 2.
Poly-Pro.
Poly-Pro.
Poly-Pro.
Poly-Pro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104046 MW; AC3E48790E223583 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496 GSSKDLAKHIRVVCDGMDLTPKIQDLKPQC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Wistar;
MEDLINE=97008156; PubMed=8855332;
                                                                                      EMBL; BC049228; AAH49228.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch
l Similarity 93.3%;
28; Conservative 1
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RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otenki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Ismono Y., Kawai-Hio Y., Sato K., Nishikawa T., Kimura K.,
A wamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H.,
RA Suzuki Y., Sugano S., Nagahari K., Takahashi-Pujii A., Oshima A.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
BR GJ, GO:0016301; F:kinase activity; IEA.
DR GJ, GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR0012019; DAGKa.
DR InterPro; IPR0012019; DAG PE-bind.
DR Pfam; PF000219; DAG PE-bind.
DR Pfam; PF000219; DAG PE-bind.
DR Pfam; PF00139; DAGKa: 1.
DR ProDom; PD012939; DAGKa: 1.
DR SWART; SW00149; ANK; 2.
DR SWART; SW0045; DAGKa: 1.
DR ROSITE; PS5088; ANK REPEAT; 2.
DR ROSITE; PS5088; ANK REPEAT; 2.
DR ROSITE; PS5088; ANK REPEAT; 2.
DR ANK Febrat: Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arsuba-tereverlum;
An intowipa K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
An intowipa K., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
An Katsuta M., Sator K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
An Kawai-Hio Y., Sator W., Ishii S., Yamamoto J., Iseono Y.,
An Kawai-Hio Y., Sator W., Nishikawa T., Kimura K., Yamashita H.,
Antsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
Anehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
BRBL, AR144599, BAGS8994.1;
BRBL, AR144599, BAGS8994.1;
CO; GO: O016301; F: Kinase activity; IEA.
BRD, AR14509; PR002110; AMK.
BRD, AR14509; DAGKa.
BREPPO: IPR00219; DAGKa.
BREPPO: IPR00219; DAGKa.
BREPPO: IPR00219; DAGKa.
BREPPO: IPR001206; DAGKa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANK repeat; Kinase.
SEQUENCE 945 AA; 106082 MW; 4DAAEA0EBD83D021 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JTL-2004 (TrEMBLrel. 27, Created)
05-JTL-2004 (TrEMBLrel. 27, Last sequence update)
05-JTL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FL742603.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 92.7%; Score 152; DB 2; Le Best Local Similarity 93.3%; Pred. No. 7.6e-13; Matches 28; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                512 GSSKDLAKHIRVVCDGMDLTPKIQDLKPQC 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD002939; DAGKa; 1.
ProDom; PD005043; DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06ZVG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
Q6ZVG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRANGE BRANGE BR
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                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ45023.
Hypothetical protein FLJ45023.
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                       SIMILARITY: Contains 2 ANK repeats, SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.
                                                                      SIMILARITY: Belongs to the eukaryotic diacylglycerol kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Phorbol-ester and DAG binding 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 152; DB 1; Length 929;
Pred. No. 7.5e-13;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R NGU; 70%49; DGKZ.

R INTERPRO; IPR002110; ANK.

R INTERPRO; IPR001216; DAGKA.

R INTERPRO; IPR001219; DAG PE-bind.

R PÉAM; PF000609; DAGK_Cat; 1.

R PÉAM; PF00781; DAGK_Cat; 1.

R PRINTS; PR01415; DAGK_Cat; 1.

R PRINTS; PR01415; DAGKZ; 1.

R PRINTS; PR00149; DAGKZ; 1.

R PRODOM; PD00549; DAGKZ; 1.

R SWART; SW00049; DAGKZ; 1.

R SWART; SW00049; DAGKZ; 1.

R SWART; SW00046; DAGKZ; 1.

R SWART; SW00046; DAGKZ; 1.

R SWART; SW00046; DAGKZ; 1.

R PROSITE; PS50297; ANK_REPEAT; 2.

R PROSITE; PS50297; ANK_REP REGION, 1.

R PROSITE; PS50297; DAG PE BIND_DOM Z; PRINSE_NEG.

R PROSITE; PS50297; ANK_REP REGION, 1.

R PROSITE; PS50297; ANK_REP R
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Catalytic-B (Potential).
ANK 1.
ANK 2.
Poly-Pro.
Poly-Lys.
Poly-Lys.
WW; 6279872004F5F38D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496 GSSKDLAKHIRVVCDGMDLTPKIQDLKPQC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                 SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D78588; BAA18942.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 93.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JC6124; JC6124.
RGD; 70929; Dgkz.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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DOMAIN DOMAIN

Q6ZT25

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Gaps

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Nature 394:697-700(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                      Kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ninomiya K., Magatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamhara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Rawai Hio Y., Satic K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Nawaho Y., Rawakami B., Suzuki Y., Sugano S., Nagahari K., Masho human cDNA sequencing project."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                        Match 92.7%; Score 152; DB 2; Length 945; Local Similarity 93.3%; Pred. No. 7.6e-13; es 28; Conservative 1; Mismatches 1; Indels
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Pred. No. 7.6e-13;
1; Mismatches 1; Indels
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ42603 is, clone BRACE3011421, highly similar to
Diacylglycerol kinase, zeta (EC 2.7.1.107).
Homo sapiens (Human).
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FL496021 fis, clone BRAWH3017180, highly similar to
Diacylglycerol kinase, zeta (EC 2.7.1.107)
                                                                                                                                                                                                                                          945 AA; 106030 MW; SEF612B9FE91F7E7 CRC64;
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SMART; SMO0248; ANK; 2.
SMART; SMO0109; Cl; 2.
SMART; SMO0045; DAGKa; 1.
SMART; SMO0046; DAGKC; 1.
PROSITE; PSS0088; ANK REPEAT; 2.
PROSITE; PSS0297; ANK_REP_REGION; 1.
ANK repeat; Kinase.
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1 Similarity 93.3%;
28; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                  Query Match
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BAC8894
DD BAC8894
DT 02-N
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Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawat-ihlo Y., Saito M., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-98379993; PubMed-9716136; DOI=10.1038/29337;
Topham M.K., Bunting M., Zimmerman G.A., McIntyre T.M.,
Blackshear P.J., Prescott S.M.;
"Protein kinase C regulates the nuclear localization of diacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ding L., Bunting M., Topham M.K., McIntyre T.M., Zimmerman G.A., Prescott S.M.; "Alternative splicing of the human diacylglycerol kinase zeta gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | FDGZ HUMAN STANDARD; PRT; 1117 AA. Q13574; 000542; 01-NOV-1997 (Rel. 35, Created) | 16-OCT-2001 (Rel. 40, Last sequence update) | 05-UU-2004 (Rel. 44, Last annotation update) | Diacylglycerol kinase, zeta (EC 2.7.1.107) (Diglyceride kinase) (DGK-2eta) (DAG kinase zeta) | NAMME-DGKZ; Synonyms-DAGK6;
                                                                                                                                                                                                                                                                                                                                                        Gaps
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J. Biol. Chem. 276:26526-26533(2001).
over 1,3-diacylglycerols, but lacks substrate specificity among molecular species of long chain diacylglycerols.
-!- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-diacylglycerol = ADP + 1,2-diacylglycerol = ADP + 1,2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                    Query Match 92.7%; Score 152; DB 2; Length 945; Best Local Similarity 93.3%; Pred. No. 7.6e-13; Matches 28; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGUENCE FROM N.A. (ISOFORM SHORT).
TISSUE=Endothelial cells;
MEDLINE=96215319; PubMed=8626588;
BuntinK=96215319, Zimmerman G.A., McIntyre T.M., Presc", Molecular cloning and characterization of a novel human
                                                                                                                                                                                                                                                          945 AA; 106082 MW; 4DAAEA0EBD83D021 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 94:5519-5524(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      512 GSSKDLAKHIRVVCDGMDLTPKIQDLKPQC 541
                                                                                                                                                                                                                                                                                                                                                                                                       1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diacylglycerol kinase zeta.";
J. Biol. Chem. 271:10230-10236(1996).
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Homo sapiens (Human)
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TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                MUTAGEN
SEQUENCE
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SMART; S
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                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its must by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Catalytic-A (Potential).
Catalytic-B (Potential).
ANK 1.
ANK 1.
ANK 2.
Poly-Pro.
Poly-Pro.
Poly-Pro.
METFRRHERGKVPGFGGGRRPSSVGLPTGKARRRSPAGQ ASSSLAQRRRSSAQLGGCLLSCGVRAQGSSRRSSTVPPSC NPRFTVDKVLTPQPTYGAQLLGAPLLLTGLYGMNEEGVQ EDVYAEASSA1QPGTKTAGGPPPRAAQPLLTGLYGMNEEGVG FORVAEASSA1QPGTKTAGGPPPRAAQPLLTGLTGLPRYVRRASS GTTAGTMLPTRVPRLSRRQVALGAPLALGAPSCAMAGALLA.
MERDGSPFARSSDSSASASSGGSRRAAGPLLA.
                                                                                                                    Isode=013574-2; Sequence=VSP_001268;

ISSUE SPECIFICITY: Highest levels in brain, and substantial

levels in skeletal muscle, heart, and pancreas.

PIM: Phosphorylation of the MARKS homology domain by PKC reduces

nuclear accumulation of DGK-zeta.

SIMILARITY: Belongs to the eukaryotic diacylglycerol kinase
 SUBUNIT: Interacts with the PDZ domain of the syntrophin SNTG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50089; ANK REPEAT; 2.
PROSITE; PS50089; ANK REPEAT; 2.
PROSITE; PS50049; DAG PE BIND DOM 1; FALSE NEG.
PROSITE; PS50041; DAG PE BIND DOM 2; FALSE NEG.
Alternative splicing; ANK repeat; Kinase; Multigene family;
Nuclear protein; Phorbol-ester binding; Phosphorylation; Repeat;
Transferase.
                                                                                                                                                                                                                                family.
SIMILARITY: Contains 2 ANK repeats.
SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R MIN, 601441; -.

R GO; GO:0005634; C:nucleus; TAS.

GO; GO:0005634; F:ATP binding; TAS.

GO; GO:0005143; F:ATP binding; TAS.

GO; GO:0001163; F:ATP binding; TAS.

R GO; GO:0001165; P:Giacy1g1ycerol kinase activity; TAS.

R InterPro; IPR001010; ANK.

R InterPro; IPR001010; ANK.

R InterPro; IPR000219; DAGKa.

R InterPro; IPR000219; DAG PE-bind.

R Pfam; PF00781; DAGK_acc; 1.

R Pfam; PF00781; DAGK_acc; 1.

R ProDom; PD002939; DAGKa; 1.

R ProDom; PD002943; DAGKa; 1.

R ProDom; PD00544; DAGKa; 1.

R SMART; SM00145; DAGKa; 1.

R SMART; SM00145; DAGKa; 1.

R SMART; SM00146; DAGKa; 1.

R SMART; SM00146; DAGKa; 1.
                SUBCELLULAR LOCATION: Nuclear and cytoplasmic. ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                     Name=Long;
IsoId=Q13574-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U51477; AAC50478.1; -. EMBL; U94905; AAE60859.1; -. Genew; HGNC:2857; DGKZ. MIM; 601441; -.
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792
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VARSPLIC
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TISSUE=Brain;

WEDLINE=22388257; PubMed=12477932;

RETARDSORDER E. Foundary Course L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bronstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rochards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., Wally D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worlley K.C., Hale S., Garcia A.M., Gab S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Althouse S.J., Marra M.A.,

Rodriguez A.C., Grimwood J., Sanmutz J., Myers R.M., Generation and initial analysis of more than 15,000 full-length human

RT and mouse CDNA sequences.",

RD Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                              Gaps
                                                1115 1116 TA->NS: Loss of interaction with SNTG1.
1117 AA; 124122 MW; 213BC8ADDB4E1402 CRC64;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                          Length 1117;
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Strauberg R.;
Strau
                                                                                                                                                              Score 152; DB 1; Length 11.
Pred. No. 9.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ol-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Diacylglycerol kinase, zeta 104kDa, isoform 2.
Name=DGKZ;
/FTId=VSP_001268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        684 GSSKDLAKHIRVVCDGMDLTPKIQDLKPQC 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 929 AA
                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30
                                                                                                                                                                                                                    Query Match
Best Local Similarity 93.3%;
Matches 28; Conservative
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PD005043; DAGKc; 1.
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; SM00109; C1; 2.
; SM00045; DAGKa; 1.
; SM00046; DAGKC; 1.
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us-10-092-750-23.rup

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EDGI HUMAN STANDARD; PRT; 1065 AA. 075212, 030749; 116-007-2001 (Rel. 40, Created) 16-007-2001 (Rel. 40, Last sequence update) 05-710-2004 (Rel. 44, Last annotation update) 1010-007-2010 (Rel. 44, Last annotation update) 1010-0710-0704 (Rel. 44, Last annotation update) 1010-0710-0710 (Rel. 44, Last annotation update) (Diacylglycerol kinase, iota (EC 2.7.1.107) (Diglyceride kinase) (DGK-iota) (DAG kinase iota).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=RELINA;
TISSUE=RELINA;
DING L., Track E., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
The cloning and characterization of a novel human diacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 2 ANK repeats.
-!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLUTAR LOCATION: Nuclear and cytoplasmic.
             LECOLD 1. Kondo H., Goto K.;

Libroral 1. Kondo H., Goto K.;

Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.

R GD, GO:0004142; P:diacylglycerol kinase activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

R GO; GO:0007262; P:procein kinase C activation; IEA.

R GI; GO:0007205; P:procein kinase C activation; IEA.

R InterPro; IPR000710; ANK.

R InterPro; IPR000756; DAGKa.

R InterPro; IPR000219; DAG Pe-bind.

R Pfam; PF00781; DAGK acc; 1.

R Pfam; PF00781; DAGK acc; 1.

R ProDom; PD00593; DAGKa; 1.

R ProDom; PD00593; DAGKa; 1.

R SYART; SM00109; C1; 2.

R SYART; SM00045; DAGKa; 1.

R SYART; SM00045; DAGKa; 1.

R SYART; SM00046; DAGKa; 1.

R RFOITE; PSS0088; ANK REPEAT; 1.

R PROSITE; PSS0088; ANK REPEAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANK repeat; Kinase. _ _ SEQUENCE 1050 AA; 115857 MW; 1D87634DB6C6643B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 72.0%; Score 118; DB 2; I Local Similarity 72.4%; Pred. No. 6.7e-08; es 21; Conservative 5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           571 SSRDLSKHVKVVCDGTDLTPKIQELKFQC 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kinase, DGK-iota.";
J. Biol. Chem. 273:32746-32752(1998).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=DGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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LISOUE-BRAIN;
LISOUE-BRAIN;
LIGORIAN CH., GOLO K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; ABG08963; BAC66895.1;
GO; GO:0004443; F:diacylglycerol kinase activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0007265; P:protein kinase C activation; IEA.
R GO; GO:0007205; P:protein kinase C activation; IEA.
InterPro; IPR001206; DAGKa.
InterPro; IPR001206; DAGKa.
R InterPro; IPR001206; DAGKa.
R Ffam; PP00609; DAGKaci.1.
R ProDom; PD005043; DAGKa; 1.
R ProDom; PD005043; DAGKa; 1.
R SWART; SW00046; DAGKa; 1.
R SWART; SW00046; DAGKa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Match 72.0%; Score 118; DB 2; Length 840; Local Similarity 72.4%; Pred. No. 5.3e-08; les 21; Conservative 5; Mismatches 3; Indels
                                                                                                                           Length 929;
                                                                                                                                                                            Indels
                                                 ANK repeat; Kinase. SEQUENCE 929 AA; 104108 MW; 56B43B9DC1FC794A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     840 AA; 92751 MW; 886D49858CB94229 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Q810C4
PRELIMINARY; PRT; 840 AA.
Q810C4;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 26, Last annotation update)
Diacylglycerol kinase iota-2.
Name=rDGXi-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Diacylglycerol kinase icta-1.
                                                                                                                     Query Match 90.2%; Score 148; DB 2; L
Best Local Similarity 90.0%; Pred. No. 2.8e-12;
Matches 27; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                           496 GSSKDLAXHIRVVCDGMDLTPKIQDLKPKC 525
                                                                                                                                                                                                                                1 GSSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30
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PROSITE; PS50088; ANK REPEAT; 2.
PROSITE; PS50297; ANK REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
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2810C4
10 0810C4
DT 01-JUI
DT 01-JUI
DT 01-JUI
DT 01-JUI
DE DE NIME STATE
OC RALKAT,
CO R
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RESULT 11

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Gaps

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Length 1050;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50088; ANK REPEAT; 2.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS50479; DAG—PE—BIND—DOM—1; FALSE_NEG.
PROSITE; PS50081; DAG—PE—BIND—DOM—2; FALSE_NEG.
ANK repeat; Kinase; Multigene—family; Nuclear protein; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phorbol-ester and DAG binding 1.
Phorbol-ester and DAG binding 2.
Catalytic-A (Potential).
Catalytic-B (Potential).
ANK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew, HGNC:2861, DGKI.

MIN, 604072;

GO, GO:0005437; C:Cytoplasm; TAS.

GO; GO:0004143; F:diacylglycerol kinase activity; TAS.

GO; GO:0004143; F:diacylglycerol kinase activity; TAS.

InterPro; IPR002110; DAGKa.

InterPro; IPR002105; DAGKa.

InterPro; IPR002203; DAGKa.

InterPro; IPR002219; DAG PE-bind.

R Pfam; PF00063; Ank; 2.

R Pfam; PF00073; Ank; 2.

R Pfam; PF00781; DAGK act; 1.

R PrDDom; PD002939; DAGKa; 1.

R ProDom; P0002939; DAGKa; 1.

R ProDom; P0002939; DAGKa; 1.

R SMART; SM0019; CI; 2.

SMART; SM0019; CI; 2.

SMART; SM00046; DAGKa; 1.
                                                                                                                                                                                                                                                                                                                                 AF219907, AAF43006.1; JOINED.
AF219908, AAF43006.1; JOINED.
AF219910; AAF43006.1; JOINED.
AF219910; AAF43006.1; JOINED.
AF219911; AAF43006.1; JOINED.
AF219911; AAF43006.1; JOINED.
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JOINED.
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AF219937; AAF43006.1; JOINED
AF219938; AAF43006.1; JOINED
                                                                                                                                                                                                                                                                            EMBL; AF061936; AAC62010.1; -. EMBL; AF219939; AAF43006.1; -.
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AF219932; AAF43006.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF43006.1;
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AAF43006.1;
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AAF43006.1;
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AAF43006.
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DOMAIN 178 2
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AF219913;
AF219914;
AF219915;
AF219916;
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AF219918;
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AF219923;
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AF219925;
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DOMAIN
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            010024; 000588; 000588; 010024; 000588; 010024; 000588; 010024; 000588; 010027-2003 [Rel. 42, Last sequence update) 010027-2003 [Rel. 44, Last annotation update) 05-JUL-2004 (Rel. 44, Last annotation update) Putative diacylglycerol kinase K06Al.6 (EC 2.7.1.107) (Diglyceride Kinase) (OK) (DAG kinase). (CK) (DAG kinase) (OK) (DAG kinase). (CK) (DAG kinase). (CK) (DAG kinase). Relapolitis elegans. Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditida; Rhabditoidea; Rhabditise.
                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-
                                                                                                                                                                                                                        Length 1065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 937;
                  Poly-Ala.
Poly-Ser.
Poly-Ala.
L -> F.
/FTIGAVAR 010190.
A -> P (in Ref. 2).
6 MW, B84971AA7630A799 CRC64;
                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Catalytic-A (Potential).
Catalytic-B (Potential).
i, 7F9FA163AF783790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fulton L.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                     Score 118; DB 1;
Pred. No. 6.8e-08;
5; Mismatches 3;
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51.7%; Pred. No. 0.0047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            937 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proom, process and pages 1.
Probom; PD002939; DAGKa; 1.
SMART; SM00045; DAGKa; 1.
SMART; SM00045; DAGKa; 1.
Hypothetical protein; Kinase; Transferase.
DOMAIN 95 157 Ser-rich.
                                                                                                                                                                                                                                                                                                                                                          576 SSRDLSKHVKVVCDGTDLTPKIQELKFQC 604
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                                                                                                                                                                             116996
                                                                                                                                                                                                                           Query Match 72.0%;
Best Local Similarity 72.4%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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1065 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418
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KDGM_CAREL
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        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=ebiG7405; ORFNames=ENSANGG0000005590;
Anopheles gambiae str. PEST.
Ebkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles Genome Sequencing Consortium, submitted (MAR-2002) to the EMBI/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBI/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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842 AA; 93307 MW; C9F570519274924D CRC64;
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EMBL; AAABO1008846; EAA06452.1; -.
GO; GO:0001413; Fidiacylglycerol kinase activity; IEA.
GO; GO:0007205; P:protein kinase C activation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSAWC90000017014 (EbiP2153).
Name=ENSANGG0000017014 (EbiP2153).
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Pred. No. 2.3;
5; Mismatches
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7; Mismatches
                                                                                                                          622 SWKDLCEYITLECDGVDVTPRIKELKLHC 650
                                                                                2 SSKDLAKHIQVVCDGMDLTPKIHDLKPQC 30
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SEQUENCE FROM N.A.
STRAIN=PEST,
Anopheles Genome Sequencing Consortium;
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PROSITE; PS50297; ANK_REP_REGION; 1.
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InterPro; IPR000756; DAGKa.
InterPro; IPR001206; DAGKc.
Pfam; PF00023; Ank; 3.
Pfam; PF00609; DAGK acc; 1.
Pfam; PF00781; DAGK_cat; 1.
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Best Local Similarity 50.0%;
Matches 12; Conservative
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ProDom; PD002939; DAGKa; 1
Conservative
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Q7QFJ1;
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Q7PCP4;
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Q7QFJ1
    Matches
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RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
RN 121
RP SECURNE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
L: Anopheles Genome Sequence shown here is derived from an CC :-: CAUTION: The sequence shown here is derived from an CC :-: CAUTION: The sequence shown here is derived from an CC :-: CAUTION: The sequence shown here is derived from an CC :-: CAUTION: The sequence shown here is derived from an CC :-: CAUTION: The sequence shown here is derived from an CC :-: CAUTION: The sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-: CAUTION: The Sequence shown here is derived from an CC :-- CAUTION: The Sequence shown here is derived from an CC :-- CAUTION: The Sequence shown here is derived from an CC :-- CAUTION: The Sequence shown here is derived from an CC :-- CAUTION: The Sequence shown here is derived from an CC :-- CAUTION: The Sequence shown here is derived from an CC :-- CAUTION: The Sequence shown here is derived from an CC :-- CAUTION: The Sequence shown here is derived from an CC :-------
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OTHER INFORMATION: Xaa=Ser or
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LOCATION: 24
OTHER INFORMATION: Xaa=1le O:
FEATURE:
NAME/KEY: UNSURE
LOCATION: 28
OTHER INFORMATION: Xaa=
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Best Local Similarity
Matches 13; Conserv
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LOCATION: 76
OTHER INFORMATION:
 FEATURE:
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LOCATION: 52
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NAME/KEY: UNSURE
   TYPE: PRT
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   Sequence 6251, Ap
Sequence 38906, A
Sequence 32311, A
Sequence 32311, A
Sequence 31724, A
Sequence 119, Appl
Sequence 14, Appl
Sequence 7, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 1060, Appl
Sequence 12730, Appl
Sequence 12730, Appli
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Sequence 12730, Appli
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12730, A
8058, Ap
1, Appli
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21, Appl
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191.991 Million cell updates/sec
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               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-270-767-38906
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US-09-270-767-32311
US-09-252-991A-30703
US-09-655-499A-31724
US-09-655-499A-31724
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US-09-10-938B-7
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1 GFLAAEQDIREEIRKVVQSLEQTAREVLTLLQG 33
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PCT-US96-01643-9
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Maximum DB
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Result

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37559, A
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163, Appl 21, Appl 21, Appl 3
7, Appl 3
7, Appl 3
7, Appl 3
7, Appl 1
7, Appl 1
1, Appl 1
1, Appl 1
1, Appl 1
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Sequence
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US-09-574-12
US-09-578-063-5
US-09-578-063-5
US-09-039-609-2
US-09-134-00C-4034
US-09-134-063-8
US-09-134-00C-4034
US-09-134-00C-4034
US-09-326-358-063-3
US-09-3817-180-2
US-09-326-358-063-3
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ALIGNMENTS

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Sequence 6251, Application US/09513999C
; Sequence 6251, Application US/09513999C
; Patent No. 6783961
; GENERAL IMFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.Y.
; APPLICANT: Giordano, J.Y.
; TILE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REPERBNCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1999-02-26
; RIOR FILING DATE: 1999-02-26
; NUMBER: OF SEQ ID NOS: 36681
; SEQ ID NO 6251
; LEWING DATE: PATENT PROTEINS
; SEQ ID NO 6251
; LEWING PATE PATENT PROTEINS
; SEQ ID NO 6251
; LEWING PATE PATENT PROTEINS
; RESERVED PATENT PROTEINS
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; SEQ ID NO 6251
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Best Local Similarity
Matches 12; Conserv
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LENGTH: 237
                         TYPE: PRT
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                                                                                                                                                                               Sequence 38906, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38906
LENGTH: 74
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GENERAL INPORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: PATENTIN Ver. 2.0
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION WUBBRS: 435/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBRS OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32311
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; Sequence 54123, Application US/09270767
; Patent No. 6703491
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Patent No. 6703491
GENERAL INFORMATION:
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; ORGANISM: Drosophila melanogaster
US-09-270-767-54123
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US-09-270-767-38906
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LENGTH: 74
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US-09-52-991A-31724

US-09-552-991A-31724, Application US/09252991A

Facence 31724, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

FEMALE APPLICATION NUMBER: US 60/094,150

FRIOR FILING DATE: 1998-07-27

FRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                               Sequence 30.703, Application US/09252991A

Sequence 30.703, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TREATURE NET OF INVENTION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30703

LENGTH: 734
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                                                                         Score 59; DB 4; Length 237; Pred. No. 2; 8; Mismatches 11; Indels
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Pred. No. 21;
7; Mismatches 9; Indels
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36.1%; Score 56;
Best Local Similarity 40.7%; Pred. No. 3
Matches 11; Conservative 7; Mismatch
; ORGANISM: Drosophila melanogaster
US-09-270-767-32311
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                                                                         Query Match
Best Local Similarity 38.7%;
Matches 12; Conservative
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| Sequence | Application US/09150867 | Sequence | Application US/09150867 | Patent No. 6645748 | Sequence | Application US/09150867 | Patent No. 6645748 | Septenct No. 6645748 | Septenct No. 6645748 | Septenct No. 6645748 | Septence | Septenc
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Patent No. 6673897

GENERAL INFORMATION:

APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL

TITLE OF INVERTION: NOVEL INHIBITORS OF NF-KappaB ACTIVATION

FILE REPERENCE: 2676-4554US

CURRENT FILING DATE: 2000-10-31

PRIOR PLILCATION NUMBER: PCT/BE99/00055

PRIOR PLILCATION NUMBER: 9201472.2

PRIOR PLILCATION NUMBER: 98201472.2

PRIOR PLILOR DATE: 1998-05-06

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1
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34.2%; Score 53; DB 4; Length 410;
Best Local Similarity 32.1%; Pred. No. 25;
Matches 9; Conservative 10; Mismatches 9; Indels
CURRENT FILING DATE: 2000-10-31
PRIOR APPLICATION WUMBER: 2000-10-55
PRIOR FILING DATE: 1999-05-05-05
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
SOFTWARE: PALENTIN NOWS: 18
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 7
LENGTH: 410
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US-09-702-953B-7
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US-09-702-953B-6
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US-09-150-867-1
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Patent No. 6610836
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
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Patent No. 6673897
BAREAL INFORMATION:
APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL TITLE OF INVENTION: NOVEL INHIBITORS OF NF-KappaB ACTIVATION FILE REFERENCE: 2676-45540S
CURRENT APPLICATION NUMBER: US/09/702,953B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

34.2%; Score 53; DB 4; Length 294;
Best Local Similarity 37.5%; Pred. No. 17;
Matches 12; Conservative 7; Mismatches 13; Indels
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36.1%; Score 56; DB 4; Length 862;
Best Local Similarity 33.3%; Pred. No. 24;
Matches 13; Conservative 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            616 GLSQAKRDVQEQMAVLMQSREQVSEELVRLQKDNDSLQG 654
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                                                                                                                                                                                                                                             Sequence 14, Application US/09665479A
Patent No. 6673570
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Itoh, Funiko
APPLICANT: Itoh, Susumu
APPLICANT: Healdin, Carl-Henrik
APPLICANT: 100-09-20
CURRENT FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
MENOTH: 862
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                               640 QDSVEQIRGVIEGLQQGTRDVVDAMHG 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Homo sapiens
US-09-665-479A-14
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US-09-489-039A-13944
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US-09-702-953B-7
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; SEQ ID NO 22
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-914-259-22
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Best Local Similarity
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US-09-538-092-1060
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                                                                                      OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E) OTHER INFORMATION: member of the kinesin superfamily of microtubule OTHER INFORMATION: motor proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2954;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.9%; Score 51; DB 4; Length 295
Best Local Similarity 50.0%; Pred. No. 5.1e+02;
Matches 12; Conservative 4; Mismatches 8; Indels
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US-00-914-259-22
Sequence 22, Application US/05914259
Sequence 22, Application US/05914259
Sequence 22, Application US/05914259
Sequence 10: Application:
APPLICANT: Makwoski, Liee
APPLICANT: Millams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REPERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09914259
Patent No. 6495336
GENERAL INFORMATION:
APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
ITILE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                          LOCATION: (1)...(472)
OTHER INFORMATION: kinesin like motor domain
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LOCATION: (2753)..(2954)
CTHER INFORMATION: tail domain
US-09-150-867-1
                                                                                                                                                                                                                                                                            LOCATION: (473)..(2752)
OTHER INFORMATION: rod domain
FEATURE:
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ORGANISM: Homo sapiens
                                                ORGANISM: Xenopus sp.
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Best Local Similarity
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NAME/KEY: DOMAIN
                                                                                                                                                    FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)..(4
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US-09-914-259-20
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LENGTH: 963
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Sequence 1230, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: GATY BRECON et. al

APPLICANT: GATY BRECON et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

FILE REFERENCE: 2709, 2004001

CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRICR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 129
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                                                                                                                                                                                                                                                                                   Sequence 1060, Application US/09538092

| Sequence 1060, Application US/09538092
| Patent No. 6753314
| GENERAL INFORMATION:
| APPLICANT: Glot, Loic
| APPLICANT: Glot, Loic
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFRENCE: 15966-542
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFRENCE: 15966-542
| CURRENT APPLICATION NUMBER: US/09/538,092
| PRIOR APPLICATION NUMBER: 60/127,352
| PRIOR FILING DATE: 2000-03-04
| PRIOR FILING DATE: 2000-02-01
| NUMBER OF SEQ ID NOS: 1387
| SOFTWARE: CURPATSESGFFORMATTER VERSION 0.9
| SEQ ID NO 1060
| LANGTH: 563
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     Length 963;
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: LoCATTON: (0)...(0)

: OTHER INDEMATION: Polypeptide Accession Number P33176

US-09-538-092-1060
ch 32.6%; Score 50.5; DB 4; 1 Similarity 44.8%; Pred. No. 1.5e+02; 13; Conservative 7; Mismatches 8;
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32.6%; Score 50.5; DB 4;
Best Local Similarity 44.8%; Pred. No. 1.5e+02;
Matches 13; Conservative 7; Mismatches 8;
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Pred. No. 16;
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45.5%;
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        Query Match
Best Local Similarity
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8; Indels Matches 10; Conservative 4; Mismatches දු ද

Search completed: November 10, 2004, 13:43:59 Job time: 12.399 secs

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Sequence 357715,
Sequence 39221, A
Sequence 3493, Ap
Sequence 44430,
Sequence 49985, A
Sequence 361021,
Sequence 6, Appli

Sequence 3332. Ap Sequence 34531, A Sequence 288907, Sequence 63666, A Sequence 219142, Sequence 61690, A Sequence 20484, A

US-10-425-115-357715
US-10-425-114-59221
US-10-128-714-8493
US-10-128-714-8493
US-10-2425-115-36.0285
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US-10-425-115-36.0285
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US-10-0806-688A-20
US-10-0806-688A-20
US-10-0806-688A-20

Sequence 20484, A Sequence 45197, A Sequence 45197, A Sequence 160703, Sequence 204556, Sequence 45413, A Sequence 45413, A Sequence 23670, A Sequence 23769, A Sequence 2418, Sequence 243, A Sequence 243, A Sequence 243, App

Sequence 20, Appl Sequence 22, Appl Sequence 109, App

ALIGNMENTS

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Sequence 24, Appl
Sequence 499, Appl
Sequence 13249, Ap
Sequence 13249, A
Sequence 22, Appl
Sequence 21, Appl
Sequence 241, Appl
Sequence 240, Appl
Sequence 236205,
Sequence 236205,
Sequence 35714, Ap
Sequence 35714, Ap
                                                                                 November 10, 2004, 16:36:12 ; Search time 35.4508 Seconds (without alignments) 328.807 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/NET_REW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/NET_REW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/NEG_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/NEG_PUBCOMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-925-297-499
US-10-102-2604-3640
US-10-1056-761-13249
US-10-437-963-106139
US-10-477-293-321
US-10-177-293-321
US-10-418-765A-2447
US-10-418-765A-2467
US-10-418-365714
US-10-425-115-236205
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155
1 GFLAABQDIREEIRKVVQSLBQTARBVLTLLQG 33
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Maximum Match 100%
Listing first 45 summaries
                                                            protein search, using sw model
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score greater than or equal to
and is derived by analysis of
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seg length: 200000000
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Match
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No.
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Gaps ö Length 33; squence 24, Application US/10092750
publication No. US20030032157A1
GENERAL INPORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia
TITLE OF INVENTION: POlypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PASCESC for Windows Version 4.0
SEQ ID NO 2 4 SEQ ID NOS: 253 Indels Query Match 100.0%; Score 155; DB 14; Best Local Similarity 100.0%; Pred. No. 3.5e-13; Matches 33; Conservative 0; Mismatches 0; 1 GFLAAEQDIREEIRKVVQSLECTAREVLTLLQG 33 TYPE: PRT
CORGANISM: Homo sapiens
US-10-092-750-24 ద à

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Sequence 499, Application US/09925297; Patent No. US20020081659A1; GENERAL INFORMATION:

US-09-925-297-499

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Query Match 36.8%; Score 57; DB Best Local Similarity 44.4%; Pred. No. 23; Matches 12; Conservative 7; Mismatches
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NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13249
LENGTH: 513
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ORGANISM: Oryza sativa
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Sequence 3640, Application US/10108260A;
Publication No. US20040005560A1;
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA;
FILE REFERENCE: HI-A0106;
CURRENT APPLICATION NUMBER: US/10/108,260A;
CURRENT FILING DATE: 2002-03-27;
NUMBER OF SEQ ID NOS: 5458;
SOFTWARE: PatentIn Ver. 2.1;
SEQ ID NO 3640;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.4%; Score 58; DB 15; Length 429; 42.9%; Pred. No. 34; tive 7; Mismatches 9; Indels
APPLICANT: Rosen et al.
TILE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAIOS PAIOS CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
FRICA APPLICATION NUMBER: PCT/US00/05989
PRICA FILING DATE: 2000-03-08
PRICA PLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOUTHARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
99.4%; Score 154; DB 9;
Best Local Similarity 97.0%; Pred. No. 5.1e-12;
Matches 32; Conservative 1; Mismatches 0
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PUBLICATION NO. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, HROSHI
APPLICANT: SHIRAWA, HROSHI
APPLICANT: SHIRAWA, HROSHI
APPLICANT: SHIRAWA, HROSHI
APPLICANT: SHIRAW, HROSHI
APPLICANT: SHIRAW, HAROSHI
APPLICANT: HATTORI, WOSHIRAWA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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| AAEAQMRQEIERLTERLEEKEREMOOLL 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 42.9°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-09-925-297-499
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US-10-108-260A-3640
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                                                                                                                                                                                                                                                                    SEQ ID NO 499
LENGTH: 253
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RESULT 5
US-10-437-963-106139
Sequence 106139, Application US/10437963
Sequence 106139, Application US/10437963
Sequence 106139, Application US/10437963
Sequence 106139, Application No. US20640123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF SERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 106139
LENCTH: 234
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Query Match 37.4%; Score 58; DB 14; Length 513; Best Local Similarity 39.3%; Pred. No. 42; Matches 11; Conservative 7; Mismatches 10; Indels
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APPLICANT: YUE, Henry; DING, Li;
APPLICANT: YUE, Huibin; HAFALIA, April J.A.;
APPLICANT: YUE, Huibin; HAFALIA, April J.A.;
APPLICANT: YUE, Huibin; HAFALIA, April J.A.;
APPLICANT: BECHA, Shanya D.; GURURAJAN, Rajagopal;
APPLICANT: BECHA, Shanya D.; GURURAJAN, Rajagopal;
APPLICANT: BECHA, Shanya D.; GURURAJAN, Narinder K.;
APPLICANT: YANG, Y. Tom; LU, Dyung Alna M.;
APPLICANT: YANG, Yalan, Jayalaxmi; GAMDHI, Ameena R.;
APPLICANT: YANG, Jumming; ELLOTT, Vicki S.;
APPLICANT: YANG, Jumming; ELLOTT, Vicki S.;
APPLICANT: HE, Ann; AZINZAI, Yalda;
APPLICANT: RAUMANN, BRIGETE E.; SWARNAKAR, Anita;
APPLICANT: RAUMANN, BRIGETE E.; SWARNAKAR, Anita;
APPLICANT: BURFORD. Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_10610C.1.pep
US-10-437-963-106139
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ghosh, Sounitra S.
APPLICANT: Ghosh, Eoin D.
APPLICANT: Tang, Bing
APPLICANT: Ghosh, Bradford W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
AUSTREE REPERRANCE: 660088 465
FURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2447
LINGTH: 862
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Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 13; Conservative 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                       9; Indels
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| APPLICANT: KEASLING, JAY |
| APPLICANT: KEASLING, JAY |
| APPLICANT: MARTIN, VINCENT |
| APPLICANT: PITERA, DIG. SER. |
| APPLICANT: WITHERS III, SYDNOR T. |
| APPLICANT: WINNAR, JACK |
| TILLE OF INVENTION: BIOSYNTHESIS OF AMORPHA-4,11-DIENE |
| FILE REFERENCE: 2000-0007.20 |
| CURRENT FILING DATE: 2000-00-09-09 |
| PRIOR APPLICATION NUMBER: 10/006,909 |
| TYPE: PATENTING DATE: 2001-12-06 |
| SOFTWARE: PATENTING PATE: 201-12-06 |
| TYPE: PRT |
| ORGANISM: Artemisia annua
                                                                                                                                                                                                                                                                                                                                                                                                    616 GLSQAKRDVQEQMAVLMQSREQVSEELVRLQKDNDSLQG 654
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                                                                                                                                                                                                                                       Query Match

36.1%; Score 56; DB 14;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 13; Conservative 11; Mismatches 9
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 391
LENGTH: 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2447, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/10411066 Publication No. US20040005678A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-408-765A-2447
                                                                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-10-177-293-391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-408-765A-2447
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APPLICANT: Bast Ur., Robert C.
APPLICANT: Meric, Funda
APPLICANT: Sahin, Ayesgul
APPLICANT: Sahin, Ayesgul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: COMPOSITION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: COMPOSITION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: COMPOSITION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: UNMBER: US 60/299,887
FILE REFERENCE: MRI-038
CURRENT PILING DATE: 2001-06-21
FRIOR APPLICATION NUMBER: US 60/306,501
FRIOR FILING DATE: 2001-09-25
FRIOR APPLICATION NUMBER: US 60/365,002
FRIOR FILING DATE: 2001-09-25
FRIOR APPLICATION NUMBER: US 60/362,585
FRIOR APPLICATION NUMBER: US 60/362,585
FRIOR APPLICATION NUMBER: US 60/362,585
FRIOR FILING DATE: 2002-03-05-65
FRIOR FILING DATE: 2002-03-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.1%; Score 56; DB 16; Length 751; Best Local Similarity 38.7%; Pred. No. 1.2e+02; Matches 12; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || :|:| | |:| |267 LAQKQEVLGQLRAHVEAAEEBARERLAELEG 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAMME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 1532441CD1
US-10-476-924-22
                                                                             PRIOR APPLICATION NUMBER: PCT/USO2/14276
PRIOR FILING DATE: 2002-05-02
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US 60/288,598
PRIOR PILING DATE: 2001-05-04
PRIOR PILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 46
SSCPID NO 22
LENGTH: 751
   FILE REFERENCE: PF-0960 USN
CURRENT APPLICATION NUMBER: US/10/476,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 391, Application US/10177293
Publication No. US20030124128A1
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Xu, Yongyao
Hoersch, Sebastian
Monahan, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
                                                                   2003-11
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ORGANISM: Homo sapiens
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Sequence 60374, Application US/10425114
; Sequence 60374, Application US/10425114
; Publication No. US20040034888A1
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Yihua
APPLICANT: Soreen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Tabaska, USC E
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313) B
; CURRENT PLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 15; Length 230;
55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: LIB3596-046-C12_FLI.pep
US-10-425-114-60374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 EQDIREEIRKVVQSLEQTAREVLTL 30
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Best Local Similarity 48.0°
Matches 12; Conservative
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Matches 12; Conservative
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
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| Publication No. US20040214272A1
| Publication No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Cano, Yihua
| APPLICANT: Cano, Yihua
| APPLICANT: Cano, Yihua
| APPLICANT: Cano, Yought
| TITLE OF INVENTION: Plants
| CURRENT APPLICATION NUMBER: US/10/425,115
| CURRENT APPLICATION NUMBER: US/20206
| NUMBER OF SEQ ID NOS: 369326
| SEQ ID NO 236205
| SEQ ID NO 236205
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US-20-425-115-357714
US-20-425
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0
                                                                     Length 551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.8%; Score 54; DB 17; Length 221; Best Local Similarity 48.0%; Pred. No. 52; Matches 12; Conservative 4; Mismatches 9; Indels
                                                                                                                                                    Indels
                                                             Query Match 35.2%; Score 54.5; DB 15;
Best Local Similarity 41.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 8; Mismatches 9;
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US-10-425-115-357714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_146C.1.pep
US-10-425-115-236205
                                                                                                                                                                                                                                  2 FLAAEQDIREEIRKVVQSL-EQTAREVLTLL 31
                                                                                                                                                                                                                                                                               24 FLAYDQDEQEGVEQVIKDLKEEVKSELLTAL 54
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Matches 12; Conservative
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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US-10-425-115-236205
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LENGTH: 221
US-10-411-066-40
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Gaps

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Sequence 43357, Application US/10767701
; Sequence 43357, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE SPERENCE: 38-21(5535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT APPLICATION NOW: 53128
SEQ ID NO 43357
LENGTH: 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C24743_1.pep
US-10-767-701-43357
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US-10-425-115-357715
US-10-425-115-357715
Sequence 357715, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , APPLICANT: La Rosa, Thomas J.
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us-10-0.

"APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic

TITLE OF INVENTION: 101-15322)

FILE REPERENCE: 38-2153222)

CURRENT PELING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 357715

TYPE: n--

TYPE: n--

TYPE: n--
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Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zorean, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Taba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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34.8%; Score 54; DB 17; Length 230;
Best Local Similarity 48.0%; Pred. No. 55;
Matches 12; Conservative 4; Mismatches 9; Indels
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/ OTHER INFORMATION: Clone ID: MRT4577_89405C.1.pep

US-10-425-115-357715
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34.8%; Score 54; DB 15;
Best Local Similarity 48.0%; Pred. No. 57;
Matches 12; Conservative 4; Mismatches 9
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; OTHER INFORMATION: Clone ID: 700209180_FLI.pep
US-10-425-114-59221
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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Search completed: November 11, 2004, 01:28:06 Job time : 36.5008 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
               Copyright
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- protein search, using sw model OM protein November 10, 2004, 12:29:32 ; Search time 7.35233 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

US-10-092-750-24 155 1 GFLAAEQDIREEIRKVVQSLEGTAREVLTLLQG 33 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	translin - human	hypothetical prima	chen	probable chemotaxi	hypothetical prote		20	3C3.10 protein - S	hypothetical prote	hypothetical prote	占	transcription init	hypothetical prote	hypothetical prote	signal-transducing	conserved hypothet	methyl-accepting c	methionyl-tRNA syn	probable integral	kinesin-related pr	hypothetical prote	gastrin-releasing	exclusion-determin	heavy	kinesin heavy chai	hypothetical prote	8	hypothetical prote	RNA 1
SUMMARIES	QI	351738	372639	E83067	183314	301281	113052	153188	110919	384387	71466	142724	4G2463	147963	372461	369452	182366	AC3214	AI1459		114156	C75487	[47010	TXBC	73	141919	711	704	\sim	1668
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oligopeptidase A-1	succinodlycan bios	hypothetical prote	probable ftsH prot	hypothetical prote	chromosome segrega	hypothetical prote	glutamate synthase	ferredoxin-depende	uncharacterized pr	hypothetical prote		hypothetical prote		ACC oxidase (clone
T49985	AB2729	C97510	C70956	A72287	B75150	C72515	T02097	C84839	C97315	G71197	F75213	G75148	A71194	866176
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m n									,					
50	0 0	20	20	20	20	49.5	49.5	49.5	49	49	49	49	49	49

ALIGNMENTS

RESULT 1

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A;Status: preliminary
A;Molecule type: mENA
A;Molecule type: mENA
A;Residues: 1-228 < AOK>
A;Cross-references: UNIPROT:Q15631; EMBL:X78627; NID:g607129; PIDN:CAA55341.1; PID:g6071: C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                      C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51738
Submitted to the EMBL Data Library, April 1994
A;Reference number: S51738
A;Accession: S51738
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GFLAAEQDIREEIRKVVQSLEQTAREVLTLLQG 33
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:TSN; TRSLN
A;Cross-references: GDB:731978; OMIM:600575
A;Map position: 10pter-10gter
translin - human
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12 GFLAAEQDIREEIRKVVQSLEQTAREILTLLQG 44

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RESULT 2 S72639
hypothetical primary sigma factor - Thermoanaerobacterium thermosulfurigenes C.Species. Thermoanaerobacterium thermosulfurigenes
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S72639

R./Matuschek, M.; Sahm, K.; Bahl, H.

submitted to the EMBL Data Library, March 1996

A.Description: Characterization of genes from Thermoanaerobacterium thermosulfurigenes EN

A.Reference number: 872635

A.Reference number: 872635

A.Accession: 572639

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-261 < MAT>
A.Residues: 1-261 < MAT>
A.Consersion: 6726972; PIDN:AAB08043.1; PID:g154;
C.Genetics:
A.Consereferences: UNIPROT:P77996; EMBL:U50951; NID:g1542972; PIDN:AAB08043.1; PID:g154;
C.Genetics:
A.Consereferences: Uniprochete probable RNA polymerase sigma factor; transcriptic F;30-255/Domain: transcription initiation factor sigma katf homology < KIF>

Gaps .. 40.0%; Score 62; DB 2; Length 261; 38.7%; Pred. No. 4.2; cive 10; Mismatches 9; Indels Query Match
Best Local Similarity 38.7%
Matches 12; Conservative

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pericentrin - mouse
(Species: Mus muscalus (house mouse)
(Species: Mus muscalus (house mouse)
(Species: Muscalus (house mouse)
(Species: Muscalus)
                                                                                        A;Accession: S01281
A;Status: translation not shown
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-115 <RIC>
A;Cross-references: UNIPROT: P09522; EMBL:X06166; NID:958808; PIDN:CAA29525.1; PID:958811
C;Superfamily: cauliflower mosaic virus DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. MOLECULE TYPE: MRNA
A. MOLECULES: 1-1920 < DDX>
A. C. TOSS-references: UNIPROT: P48725; GB: U05823; NID: 9458667; PIDN: AAA17886.1; PID: 9458668
C. Keywords: coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: DC3G
A,Cross-references: FlyBase:FBgn0026145
A,Map position: X
F;1147-1376/Domain: CDC2S-type guanine nucleotide exchange activator homology <SOS>
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Moleoule type: mRNA
A,Residues: 1-1383 <1SH>
A,Cross-references: EMBL:AF053358; NID:g3582764; PID:g3582765; PIDN:AAC35280.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             guanine mucleotide exchange factor DC3G - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #text_change 15-Mar-2004 C;Accession: T13052 R;Ishimaru, S;; Gaul, U; Hanafusa, H; Sibhimaru, C;Accesion: Data Library, March 1998 A;Description: CDNA sequence of Drosophila melanogaster DC3G gene. A;Reference number: 217593
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Nucleic Acids Res. 15, 8451-8466, 1987
A,Title: Sequence of figwort mosaic virus DNA (caulimovirus group)
A,Reference number: S01279; MUID:88040466; PMID:3671088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1383;
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ilarity 43.5%; Pred. No. 2.2e+02;
Conservative 5; Mismatches 8;
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Best Local Similarity 47.6%; Pred. No. 12;
Matches 10; Conservative 7; Mismatches
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Pred. No. 3e+02;
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Best Local Similarity
Matches 10; Conserv
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A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2654
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A,Experimental source: strain PAO1
C,Genetics:
A,Gene: PA4633
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hypothetical protein 3 - figwort mosaic virus
C;Species: figwort mosaic virus
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S01281
R;Richins, R.D.; Scholthof, H.B.; Shepherd, R.J.
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                                                                                    ; Score 56; DB;
; Pred. No. 62;
7; Mismatches
                                                    LAAEQDIREEIRKVVQSLEQTAREVLTLLQG 33
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Best Local Similarity 40.7%;
Matches 11; Conservative
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A;Molecule type: DNA
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Matches

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Lranscription initiation factor sigma sigA [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accesson: AG2463
BNA Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Title: Accession: AG2463
A,Cross-references: UNIPROT:084819, GB:AE001354, GB:AE001273, NID:g3329280, PIDN:AAC6840!
A,Experimental source: serotype D, strain UM-3/Cx
C;Genetics:
A,Gene: CT813
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A,Status: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1.390 GBRA-
A,Cross-references: UNIPROT: P26683; GB:M60046; NID:g142107; PIDN: AAA22043.1; PID:g142108
C,Superfamily: transcription initiation factor sigma 43; transcription initiation factor C,Keywords: DNA binding; sigma factor; transcription initiation
F;160-385/Domain: transcription initiation factor sigma katf homology <KTF>
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C;Superfamily: transcription initiation factor sigma 43; transcription initiation factor
C;Keywords: transcription initiation
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;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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33.5%; Score 52; DB
Best Local Similarity 34.8%; Pred. No. 65;
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A;Molecule type: DNA
A;Residues: 1-390 <KUR
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B84387
hypothetical protein Vng2366c [imported] - Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Dates: N
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C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Change 09-Ju1-2004
C;Accession: F71466
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, A;Tite: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachine cenome sequence of an obligate intracellular pathogen of humans: Chlamydia trachine cenomes: A71570; MUID:99000809; PMID:9784136
A;Accession: F71466
A;Accession: F7
                                                                        3C3.10 protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 16-Jul.-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T10919 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 R;Perskinl: J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1998 A;Reference number: Z17215 A;Reference number: Z17215 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-124 <PAR> A;Residues: 1-124 <PAR> A;Residues: 1-124 <PAR> A;Residues: 1-124 <PAR> A;Experimental source: strain A3(2) A;Genetics: A;Gen
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33.5%; Score 52; DB 2; Length 182;
Best Local Similarity 43.3%; Pred. No. 44;
Matches 13; Conservative 5; Mismatches 12; Indels
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A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Shith, H.O.; Wosse, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaech. A; Reference number: A69250; MUID:98049343; PMID:9389475
                        C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47963
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet submitted to the Protein Sequence Database, January 2000
A;Reference number: Z24480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein APE2336 - Aeropyrum pernix (strain Kl)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72461
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Vamazaki, J.; Kayafiel: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
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AjMolecule type: DNA
AjMolecule: 1-467 «KMA»
AjCross-references: UNIPROT:Q9Y9F2; DDBJ:APC00064; NID:g5105945; PIDN:BAA81348:1; PID:d1
AjExperimental source: strain Kl
CjGenetics:
AjGene: APE2336
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: OS-Dec-1997 #sequence_revision OS-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69452
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum.
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Pred. No. 1.1e+02;
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33.5%; Score 52; DB 2; Length 467
Best Local Similarity 45.8%; Pred. No. 1.2e+02;
Matches 11; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                  A;Residues: 1-443 <DEH>
A;Cross-references: UNIPROT:Q9M367; EMBL:AL132959
A;Experimental source: cultivar Columbia; BAC clone F15G16
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 3
A;Introns: 51/1; 166/3; 223/3; 265/2; 281/3; 334/3; 363/2
A;Note: F15G16.100
hypothetical protein F15G16.100 - Arabidopsis thaliana
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40.0%; Pred. No. 1...
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Best Local Similarity 40.09
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A;Molecule type: DNA
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A,Accession: C69452
A,Status: preliminary; nucleic acid sequence not shown; translation not shown.
A,Ketatus: preliminary; nucleic acid sequence not shown; translation not shown.
A,Kesicus: 1-781 «KLB»
A,Cross-references: UNIPROT:028653; GB:AE000990; GB:AE000782; NID:g2689313; PIDN:AAB89622
A,Cross-references: UNIPROT:028653; GB:AE000990; GB:AE000782; NID:g2689313; PIDN:AAB89622
Query Match
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 12; Conservative 9; Mismatches 12; Indels 6; Gaps 1;
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Search completed: November 10, 2004, 13:40:34 Job time : 9.35233 secs

us-10-092-750-24.rup

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model	
Run on: November 10, 2004, 12:27:34 ; Search time 40.2953 Seconds (without alignments)	<pre></pre>

US-10-092-750-24 155 1 GFLAAEQDIREEIRKVVQSLEQTAREVLTLLQG 33 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P97891 cricetulus	O15631 homo sapien	E D	Q71sy3 rattus norv	Aaf60295 mus muscu	Aaf91387 rattus no	nus mo	sndou	xenopus		rattus		thermoanae	nopheles	Q6df92 xenopus lae	Q9v5m0 drosophila	ethanos	Q882z8 setaria ita	Q815u7 bacillus ce	Q74eu4 geobacter s	Aar34195 geobacter	ycoi	Q71512 homo sapien	ощо	01101	þ	trept	Q6yzi7 oryza sativ	130 oryza	7 £m8 v	nvf8 pseudom
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Query Match
Best Local Similarity 97.0%; Pred. No. 1.8e-09;
Matches 32; Conservative 1; Mismatches 0; Indels

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Qémq85 bdellovibri Cae78562 bdellovibri Q8868 pseudomonas Q81459 bacillus ce Q91432 caenorhabdi Q6100 candida gla Q91014 pseudomonas Q95072 homo sapien Q9572 homo sapien Q15276 homo sapien Q15551 mus musculu Q35551 cattus norv Q77af6 mycoplasma			ata; Euteleostomi; ridae; Cricetinae;	latabases. ally recognizes ilons in chromosomal	Julin (19/) local assingle-stranded DNA g at recombination hot ructure (By similarity).	oration on in merci	(Potential). F69C CRC64;
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36.5 36.5 36.5 36.5 36.1 36.1 36.1 36.1 36.1 36.1 36.1 36.1	STANDARD;	(Rel. 38, (Rel. 38, (Rel. 44,	riseus etazoa theria 0029;	ary; (MAY-1996) to t ION: DNA-binding nsus sequences a	tor gene segment generated by and (By similarity) IT: Forms a mult LLULAR LOCATION: ARITY: Belongs t	This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinfo the Buropean Bioinformatics Institute. Use by non-profit institutions as low modified and this statement is not remoenties requires a license agreement or send an email to license@isb.shb.ch)	EMEL; X98066; CAA66663.1; HSSP; Q62348; IKEY. INTERFYCT: IFRO2848; Translin. Pfam; PF01997; Translin; 1. DNA-binding; Muclear protein. DOMAIN 177 198 SEQUENCE 228 AA; 26171 MW;
6 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1 TSN CRIGR ID TSN CRIGR	AC P9/891; DT 15-JUL-1999 DT 15-JUL-1999 DT 05-JUL-2004	DE Translin. GN Name=TSN; OS Cricetulus grise; OC Bukaryota; Metazo OC Mammalia; Buther OC Cricetulus. OX NCBI_TaxID=10029	SEO TISO SEO SEO SEO SEO SUD		CC This SWIS CC between CC the Burop CC use by CC modified CC modified CC entities	

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RESULT 3
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XX TISSUE-LUNG;

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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Attaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Attschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Attschul S.F., Joederg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haish F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haish F.,

A Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,

Rada S.S., Morley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

A Villalon D.K., Muray D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schall J.E., Jones S.J.M., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schall J.E., Jones S.J.M., Marra M.A.,

RA Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kasai M., Matsuzaki T., Katayangi K., Omori A., Maziarz R.T., Strominger 'U., Aoki K., Suzuki K.; Strominger 'U., Aoki K., Suzuki K.; The translin ring specifically recognizes DNA ends at recombination hot spots in the human genome."; Jablo. Chem. 27:11402-11407(1997).

-1. FUNCTION: DNA-binding protein that specifically recognizes consensus sequences at the breakpoint junctions in chromosomal translocations, mostly involving immunosipobulin (Is)/T-cell receptor gene segments. Seems to recognize single-stranded DNA ends generated by staggered breaks occuring at recombination hot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakahara K., Kasai M.;
localization of the gene encoding
                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                  "A novel gene, Translin, encodes a recombination hotspot binding protein associated with chromosomal translocations."; Nat. Genet. 10:167-174(1995).
                                                                                                                                                                                                                                                                 MEDLINE-95392568; PubMed-7663511;
Aoki K., Suzuki K., Sugano T., Tasaka T., Nakahara K., Kuge O.,
Omori A., Kasai M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 23-215 FROM N.A.
MEDLINE=97386594; PubMed=9244443;
Acki K., Inazawa J., Takahashi T., Nakahara K., Kasai "Genomic structure and chromosomal localization of the translin, a recombination hotspot binding protein.", Genomics 43:237-241(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                         Last sequence update)
Last annotation update)
                                      228 AA
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97269049; PubMed=9111049;
                                                                        Created)
                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                      15-JUL-1999
15-JUL-1999
01-OCT-2004
                                    TSN HUMAN
Q15631;
                                                                                                                             Translin.
                                                                                                                                                  Name=TSN;
                                                                                                                                                                                                                                                       SEQUENCE
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SUBUNIT: Forms a multimeric ring-shaped structure.

-!- SÜBUNIT: Forms a multimeric ring-shaped stru -!- SUBCELLULAR LOCATION: Nuclear. -!- SIMILARITY: Belongs to the translin family.

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CSTRAIN=FIVB/N, ISSUE=Mammary gland;
MEDLINE=22389257; Pubbmed=1247932; DOI=10.1073/pnas.242603899;
KRIAUSE-22389257; Pubbmed=1247932; DOI=10.1073/pnas.242603899;
KRIAUSE-22389257; Pubmed=1247932; DOI=10.1073/pnas.242603899;
KRIAUSE-EX. L. Feingold E.A., Grouse L.H., Derge J.G.,
Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Alschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MBDLINE=97386594; PubMed=9244443;
Aoki K., Inazawa J., Takahashi T., Nakahara K., Kasai M.;
"Genomic structure and chromosomal localization of the gene encoding
translin, a recombination hotspot binding protein.";
Genomics 43:237-241(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 1.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                MIM, 600575, -.

GO, GO:0005634; C:nucleus; TAS.

GO, GO:0003677; F:DNA binding; TAS.

GO, GO:0005100; P:DNA recombination; TAS.

InterPro; IPR002848; Translin.

Pfam; PF01997; Translin; 1.

10-structure; DNA-binding; Nuclear protein.

11-198 Leucine-zipper (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GFLAAEQDIREEIRKVVQSLEQTAREVLTLLQG 33
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Last annotation update)
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                                                                                                                 EMBL; X78627; CAA55341.1; --
EMBL; BC002359; A4402359.1; --
EMBL; Y12563; CAA73150.1; JOINED.
EMBL; Y12564; CAA73150.1; JOINED.
EMBL; Y12565; CAA73150.1; JOINED.
EMBL; Y12565; CAA73150.1; JOINED.
EMBL; Y12567; CAA73150.1; JOINED.
PIR; S51738; S51738.
PDB; JUJU; X-RAY; A/B/C/D=1-228.
Genew; HGNC:12379; TSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           062348;
15-701-1999 (Rel. 38, Created)
15-701-1999 (Rel. 38, Last seq
01-0CT-2004 (Rel. 45, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.4%;
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Best Local Similarity 97.0
Matches 32; Conservative
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SEQUENCE FROM N.A.
Chemnathukuzhi V.M., Lefrancois S., Morales C.R., Syed V., Hecht N.B.;
Elevated levels of the polyadenylation factor CstF 64 regulate the
alternative processing of Testis Brain RNA-binding protein (TB-RBP)
pre-mRNA in male germ cells.";
Sübmitted (FBE-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF5234179; AAF60295.1;
SEQUENCE 228 AA, 26201 MW; 39FBB4FCC5AA375C CRC64;
                                                                                                                                                                                      Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                             STRAIN-Sprague-Dawley, TISSUB-Brain, MEDLINE-98344761; PubMed-9681436; Taira E., Finkenstadt P.M., Baraban J.M., "Identification of translin and trax as components of the GS1 strand-specific DNA binding complex enriched in brain."; Jeurochem. 71:471-477 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1.0CBI_TaxID=10090;
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STRAIN=Spraque-Dawley; TISSUE-Brain;
Alia B., Finkenstadt P.M., Baraban J.M.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF062356; AAF91387.1; -
InterPro; IPR002848; Translin.
Pfan; PF01997; Translin. 1.
SEQUENCE 228 AA; 26171 MW; 29AAFDB45D73F69C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                        05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 1.8e-09;
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99.4%; Score 154; DB 2;
Best. Local Similarity 97.0%; Pred. No. 1.8e-09;
Matches 32; Conservative 1; Mismatches 0
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AAF91387;
02-MAR-2004 (TrEMBLrel. 27, Created)
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Best Local Similarity 97.0%;
Matches 32; Conservative
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                                                                                                                                                                     Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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AAF60295
ID AAF60295
AC AAF60295;
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AAF91387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                              and mouse CDNA sequences.",
Proc. Natl. Acad. S21. U.S.A.
Proc. Natl. Acad. S21. U.S.A.
-!- FUNCTION: DNA-binding protein that specifically recognizes
-!- CONSENSUS SEQUENCES at the breakpoint junctions in chromosomal
translocations, mostly involving immunoglobulin (Ig)/T-cell
receptor gene segments. Seems to recognize single-stranded DNA
ends generated by staggered breaks occuring at recombination hot
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PDB; IXEY; X-ray; A/B/C/D=1-228.
MGD; MG1:109263; TC:0ytoplasm; IDA.
GG; GG:0005737; C:0ytoplasm; IDA.
GG; GG:0005515; F:protein binding; IPI.
GG; GG:0003723; F:RNA binding; IPI.
R GG; GG:0003723; F:RNA binding; IDA.
R Pfam; PF01997; Translin; IDA.
W 3D-structure; DNA-binding; Nuclear protein.
FDOMAIN 177 198
Leucine-zipper (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Forms a multimeric ring-shaped structure. SUBCELLULAR LOCATION: Nuclear. SIMILARITY: Belongs to the translin family.
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EMBL, Y12569; CAA73151.1, JOINED.
EMBL, Y12570; CAA73151.1, JOINED.
EMBL, Y12571; CAA73151.1, JOINED.
EMBL, Y12572; CAA73151.1, JOINED.
EMBL, BC004615, AAH04615.1;
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Best Local Similarity 97.0
Matches 32; Conservative
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216
228 AA;
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Matches 32; Conserv
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                                                                                                                            STRAIN=C57BL/6J
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Q7ZXK0;
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Q7ZXK0
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                                                                                                                                                                                                  MEDLINE=98344761; PubMed=9681436; Taira E., Finkenstadt P.M.; Baraban J.M.; Taira E., Finkenstadt P.M.; Baraban J.M.; Ishenstion of translin and trax as components of the GS1 strand-specific DNA binding complex enriched in brain."; J. Neurochem. 71:471-477(1998).
                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCB1_TaxID=10116;
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14-ARR-2004 (TrEMBLrel. 27, Last sequence update)
14-ARR-2004 (TrEMBLrel. 27, Last annotation update)
ES cells CDNA, RIKBN dull-length enriched library, clone:2410083E08
product:translin, full insert sequence.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=brain;
Taira E., Finkenstadt P.M., Baraban J.M.;
Submitted (MAY-2000 to the EMBL/GenBank/DDBJ databases.
EMBL, AF265556; AAF91387.1; -
SEQUENCE 228 AA; 26171 MW; 29AAFDB45D73F69C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    .
; 29AAFDB45D73F69C CRC64;
02-MAR-2004 (TrEMBLrel. 27, Last sequence update) 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 154; DB 2; I
Pred. No. 1.8e-09;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFLAAEQDIREEIRKVVQSLEQTAREVLTLLQG 33
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Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 AA.
                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J;
MEDLINE=22354683; PubMed=12466851;
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MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meth. Enzymol. 303:19-44(1999)
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BAB27152;
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GTRAIN-CSTBL/60;
Adachi d', Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi d', Aizawa K., Akahira S., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A hanagaki T., Hana A., Hayatsu N., Hiramoto K., Hiraoka T., Rato H.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konon H., Kouda M., Koya S., Kurihara C.,
A matsuyama T., Miyazaki A., Mishi K., Nomura K., Numazaki R., Ohno M.,
Antsuyama T., Miyazaki A., Mishi K., Nomura K., Sakai C., Saki K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Antsameteu J., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Antsameteu M., Hayashizaki Y.,
Antsameteu M., Hayashizaki Y.,
Antsameteu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO10737; BAB27152.1;
SEQUENCE 228 AA; 26201 MW; 39FBB4FCCSAA375C CRC64;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
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                                                                                                                                                                                                                                                                                      MEDLINE=2033013; PubMed=11076861; Magacka S., Sasaki N., Carninci P. Shibata K., Itoh M., Aizawa K., Nagacka S., Sasaki N., Carninci P. Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Innue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J. Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Saraki Y., Ishikawa T., Alayashizaki Y., Sequencing pipeline with 384 multicapillary sequencer.";
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 1.8e-09;
1; Mismatches 0;
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Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                  Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-binding protein that specifically recognizes consensus sequences at the breakpoint junctions in chromosomal translocations, mostly involving immunoglobulin (Ig)/T-cell receptor gene segments. Seems to recognize single-stranded DNA ends generated by stagered breaks occuring at recombination hot spots (By similarity).
-!- SUBUNIT: Forms a multimeric ring-shaped structure (By similarity).
-!- SUBCELIULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the translin family.
                                                                                                                    Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN 177 198 Leucine-Zipper (Potential). SEQUENCE 229 AA; 25960 MW; E1DB50693A84D2C9 CRC64;
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Last annotation update)
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                 Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002848; Translin.
Pfam; PF01997; Translin; 1.
DNA-binding; Nuclear protein
DOMAIN 177 198
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                   15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
05-JUL-2004 (Rel. 44,
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                   Translin.
                                                                                                     Name=TSN
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Maddan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smallus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                             Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                      "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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83.2%; Score 129; DB 2; Length 22
Best Local Similarity 83.9%; Pred. No. 1.2e-06;
Matches 26; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.2%; Score 129; DB 2; Length 15
83.9%; Pred. No. 8.1e-07;
ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: BC004957; AA44957.1; -.
HSSP; Q62348; IXEY.
InterPro; IPR002248; Translin.
Pfam; PF01997; Translin; 1.
SEQUENCE 154 AA, 17780 MW; ECDD4710067BF486 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Lorca T., Castro A., Labbe J.-C.;
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF169343; AAF65620.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR002848; Translin.
Pfam; PF01997; Translin; 1.
SEQUENCE 228 AA; 26294 MW; A306DCC2ED5CE6E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUM-2001 (TrEMBLrel. 17, Last annotation update)
Translin.
                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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MEDLINE=22341132; PubMed=12454917;
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                                                                                                                                                                                                                                                                                                                              initiative.";
Dev. Dyn. 225:384-391(2002)
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Best Local Similarity 83.9<sup>3</sup>
Matches 26; Conservative
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TISSUE=Embryo;
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5 AEQDIREEIRKVVQSLEQTA-REVLTLL 31
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EMBL; AAAB01008982; EAA43447.1; -.
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Best Local Similarity 53.0.
Best 15; Conservative
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01-MAR-2004
01-MAR-2004
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Matches
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Q6DF92
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Submitted (MAK-1996) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are than released (By similarity).
-!-SIMILARITY: Belongs to the sigma-70 factor family.
EMBL; U50951; AAB08043.1; -..
BIR; S72639; S72639.
GO: GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
                                   Gaps
                                                                                                                                                                                                  AgCP6534 (Fragment).

Name=agCG53365; ORFNames=ENSANGG0000019317;

Anopheles gambiae str. PEST.

Elwaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                       Anopheles Genome Sequencing Consortium;
Submittend (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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           DB 2; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales, Thermoanaerobacteriaceae, Thermoanaerobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 287 AA; 32023 MW; DODADOF56C5B9037 CRC64;
                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P77996 PRELIMINARY; PRT; 261 AA. P77996; D77996; D1-FBB-1997 (TrEMBLrel. 02, Last sequence update) 01-FBB-1997 (TrEMBLrel. 02, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermoanaerobacter thermosulfurogenes (Clostridium
                                                        4 AAEQDIRE----EIRKVVQSLEQTAREVLTLLQG 33
                                                                     57. AARQASRRAARAPEIRKVVQSLEQTAREILTILLQG 91
          65.5%; Score 101.5; DB 2
71.4%; Pred. No. 0.0018;
iive 1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
45.8%; Score 71; DB 2;
Best Local Similarity 41.9%; Pred. No. 5.2;
Matches 13; Conservative 8; Mismatches 1
                                                                                                                                          287 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FLAAEQDIREEIRKVVQSLEQTAREVLTLLQ 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                 EMBL; AAABO1008960; EAA11822.1; -. InterPro; IPR002848; Translin. Pfan, Pfan, Pfan, Pfan, Pfan, Pfan, Pfan, Pfoly.
                                                                                                                                                            01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                 25; Conservative
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thermosulfurogenes)
                      Similarity
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=EM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=33950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sigma factor.
                                                                                                                                                                                                                                                                                              STRAIN=PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=siqA
            Query Match
                      Best Local
Matches 2
                                                                                                                                          070729
                                                                                                                RESULT 12
Q7Q729
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P77996
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GO; GO:0016987; F:sigma factor activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:000635; P:requiation of transcription, DNA-dependent; IEA.

RG); GO:000635; P:requiation of transcription, DNA-dependent; IEA.

GO; GO:000635; P:requiation of transcription, DNA-dependent; IEA.

RO; GO:000635; P:transcription initiation; IEA.

RO; GO:000635; P:transcription initiation; IEA.

RINTEPTO; IPRO00643; RNA_DOL_sigma.

RINTEPTO; IPRO00643; Sigma70_r2.

RINTEPTO; IPRO00643; Sigma70_r2.

RP Ffam; PF04542; Sigma70_r2; I.

RP Ffam; PF04542; Sigma70_r3; I.

RP Ffam; PF04545; Sigma70_r3; I.

RP ROSITE; RO00716; SIGMA70_r3; I.

RP ROSITE; PS00715; SIGMA70_r1; I.

RP ROSITE; PS00716; SIGMA70_l; I.

RM -binding; DNA-directed RNA polymerase; Sigma factor;

Transcription regulation; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles Genome Sequencing Consortium, Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MRR-2004 (TrEMBLrel. 26, Created)
01-MRR-2004 (TrEMBLrel. 26, Last sequence update)
101-MRR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGRO00000225590 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
10-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 40.0%; Score 62; DB 2; Local Similarity 38.7%; Pred. No. 49; es 12; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139
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Richards R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Eather N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Eather D.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carannor T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toodhyuki S., Carninci P., Frange C.,
Brasa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broax S.A., McZwan P.J., McKernan K.J., Maake J.A., Gubbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
And Whiting M., Madan A., Young A.C., Sheckchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Andring M. Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,
Andrinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Adnes S.J., Marra M.A.,
Andre M. M. Schmitz J., Wyers R.M., Butterfield Y.S.,
Andre S.J., Marra M.A.,
Andre S.J., Marra M.J., Marra M.J.,
Andre S.J.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Ocytes;
Klein S., Strausberg R.;
Klein S., Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC076849; AAH76849.1; -.
Hypothetical protein.
SEOUENCE 325 AA; 36819 MW; 524E146968D3B37C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.7%; Score 60; DB 2;
44.8%; Pred. No. 1e+02;
tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-Occytes;
MEDLINE-22341132; PubMed=12454917;
                                                                                                                                                                                                    TISSUE=Occytes;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
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Best Local Similarity 44.8
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxID=8355;
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Search completed: November 10, 2004, 13:38:19 Job time : 42.2953 secs

1 GFLAAEQDIREEIRKVVQSLEQTAREVLT 29

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Gaps

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9; Indels

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us-10-092-750-25.rai

Appli

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Sequence of Sequen
                                                       Sequence 2807, Ap Sequence 18231, A Sequence 18231, A Sequence 2, Appli Sequence 20767, A Sequence 291, App Sequence 16, Appl Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42036, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42036
LENGTH: 510
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Sequence 16,
                             Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 31.0%; Score 52; DB 4; Length 510; Best Local Similarity 36.7%; Pred. No. 8.4; Matches 11; Conservative 6; Mismatches 5. Talana
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                                                4 VKDVLILSALRRMLWAADDFLEDLPFEQIG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || :::|:| :| :| | | 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Drosophila melanogaster US-09-270-767-42036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.8%;
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ORGANISM: Candida albicans
   409
2552
3314
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11588
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JS-09-248-796A-14421
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44.5
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7, Appli
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5100, Ap
                                                                                                                                                                                                      November 10, 2004, 12:32:37 ; Search time 11.399 Seconds (without alignments)
191.991 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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Sequence
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1. /ogiZ_6/prodata/1/iaa/5A_COMB.pep:*

2. /ognZ_6/prodata/1/iaa/5B_COMB.pep:*

3. /ognZ_6/prodata/1/iaa/6A_COMB.pep:*

3. /ognZ_6/prodata/1/iaa/BaCOMB.pep:*

3. /ognZ_6/prodata/1/iaa/PCTUS_COMB.pep:*

5. /ognZ_6/prodata/1/iaa/PCTUS_COMB.pep:*

6. /ognZ_6/prodata/1/iaa/PCTUS_COMB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-270-767-42036
US-09-134-0706-14421
US-08-134-0706-601
US-08-801-308-1
US-08-801-308-1
US-08-935-093A-2
US-08-765-856-4
US-08-765-856-4
US-09-711-164-3633
US-09-489-039A-8330
US-09-252-991A-24606
US-09-252-991A-24606
US-09-252-991A-31958
US-09-252-991A-31958
US-09-398-550-4
US-09-398-550-4
US-09-398-550-4
US-09-398-550-4
US-09-398-550-4
US-09-762-724-10
US-08-972-902-7
US-09-972-902-7
US-09-134-001C-5100
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US-09-248-796A-15599
US-09-328-352-4504
US-10-101-464A-829
                                                                                                                                                                                                                                                                                                                                  US-10-092-750-25
168
1 LDPVKDVLILSALRRMLWAADDFLEDLPFEQIG 33
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-09-134-001C-5100
-09-489-039A-10307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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48.5
48.5
48.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
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: 1404 amino acids
amino acid
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US-08-935-009A-2
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US-08-765-856-2
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GENERAL INFORMATION:

APPLICANT: SCOLL, ROBERT E.

TITLE OF INVENTION: CDNA ENCODING P2P PROTEINS AND USE OF

TITLE OF INVENTION: P2P CDNA-DERIVED ANTIBODIES AND ANTISENSE REAGENTS IN

TITLE OF INVENTION: DETERMINING THE PROLIFERATIVE POTENTIAL OF NORMAL,

TITLE OF INVENTION: ABNORMAL AND CANCER CELLS IN ANIMALS AND HUMANS

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT LYNN DOUGETE-Stamm et al
APPLICANT LYNN DOUCETE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE: 032796-0323
CURRENT APPLICATION NUMBER: US/09/134,000C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                     Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PACENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/801,308
FILING DATE: 18-FEB-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: Weiser & Associates, P.C.
: 230 S. Fifteenth Street, Suite 500
Philadelphia
                                                                                           291 VKSVLQLLLIQSLSELFESDDFYENVPYDYL 321
                                                              4 VXDVLILSALRRM--LWAADDFLEDLPFEQI 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49.5; D
Pred. No. 11;
8; Mismatches
Best Local Similarity 35.5%; Pred. No. 17; Matches 11; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 DVLILSALRRMLWAADDFLEDLPFEQI 32
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SEGTWARE: Patentin version 3.1
SEQ ID NO 6601
LENGTH: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372.6435P
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Patent No. 6617156
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Patent No. 6368790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Welser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 372.
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT

ORGANISM: Enterococcus faecalis
US-09-134-000C-6601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.5%;
Best Local Similarity 40.7%;
Matches 11; Conservative 
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                      US-09-134-000C-6601
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                                                                            29.5%; Score 49.5; DB 3; Length 1404; 31.6%; Pred. No. 71; Live 8; Mismatches 11; Indels 7;
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CITY: ADDOLT PAIK
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,856
FILING DATE: 27-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: A24
PRIOR APPLICATION: A24
REGISTRATION: DATA:
APPLICATION NUMBER: PCT/IT95/00073
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weinstein. David L.
REGISTRATION NUMBER: 28,128
REFERENCE/DOCKET NUMBER: 5750.US.O1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
29.2%; Score 49; DB 3; Length 300;
Best Local Similarity 38.5%; Pred. No. 13;
Matches 10; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                        3 PVKDVLILSALRRMLWAADDF---LEDL----PFEQIG 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
TOPOLOGY: li-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (847) 937-6182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO: 2:
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                                                                               Query Match
Best Local Similarity 31.6'
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Protein US-08-765-856-2
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-801-308-1
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VESULA SECULATION OF APPLICATION US/08935009A

Sequence 4, Application US/08935009A

Sequence 4, Application US/08935009A

Sequence 4, Application US/08935009A

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: US

COUNTRY: US

ZIP: 60064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                      SOFTWARE: PERCENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/76,856
FILING DATE: 27-DEC-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/1T95/00073
FILING DATE: 15-MAY-1995
ATTORNEY/AGBNT INPORMATION:
NAME: Weinstein, David L.
REGISTRATION NUMBER: 28,128
REFERENCE/POCKET NUMBER: 28,128
REFERENCE/POCKET NUMBER: 5750.US.O1
TELECOMOUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 DTLLYVASRNGLFAVENFLTEEPFQR 143
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COPERATION SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,009A
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NAME: Weinstein, David L
REGISTRATION NUMBER: 28, 128
REFERENCE/DOCKET NUMBER: 618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-6182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                          TELEFAX: (847) 938-2623
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 847-937-61
TELEFAX: 847-938-2623
         OPERATING SYSTEM:
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Batent No. 6074817
GENERAL INFORMATION:
APPLICANT: Landini, Maria P.
APPLICANT: Ripalti, Alessandro
APPLICANT: Maine, Gregory T.
TITLE OF INVENTION: RECOMBINANT MONO AND POLY ANTIGENS TO DETECT CYTOMEGALOVIRUS-S
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
Sequence 2, Application US/08935009A
Patent No. 6177241
GENERAL INFORMATION:
APPLICANT: Maine, Gregory T.
TITLE OF INVENTION: SPECIFICITY OF AN ENZYME IMMUNOASSAY FOR
TITLE OF INVENTION: THE DETECTION OF HERPESVIRUS SPECIFIC IGM ANTIBODY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOSTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,009A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORIEST AGENT INFORMATION:
NAME: Weinstein, David L
REGISTRATION NUMBER: 28,128
REFERENCE/DOCKET NUMBER: 6186
TELECOMMUNICATION INFORMATION:
TELECHONE: 847-937-6182
TELEFAX: 847-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 300 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 38.54
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                          CITY: Abbot
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US-08-765-856-4
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Sequence 131584, Application US/09252991A

Sequence 131584, Application US/09252991A

Patent No. 6551755

GENERAL INFORMATION:

PAPLICANT: MATE J.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 366
                                                                    Sequence 24606, Application US/09252991A

Sequence 24606, Application US/09252991A

Sequence 24606, Application US/09252991A

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERBENCE: 107196.128

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

SEQ ID NO 24606

LENGTH: 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
28.6%; Score 48; DB 4; Length 366;
Best Local Similarity 40.0%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
28.9%; Score 48.5; Di
Best Local Similarity 40.0%; Pred. No. 21;
Matches 12; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 PVNDLALL------DPRLTDLPFEQL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PVKDVLILSALRRMLWAADDFLEDLPFEQI 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 PVKGLYFWGGVGRGKTYLVDTFFESLPFEQ 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PVKDVLILSAL-RRMLWAADDFLEDLPFEQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 506, Application US/08936165A Patent No. 6348582 GENERAL INFORMATION: APPLICANT: Black, Michael APPLICANT: Burnham, Martin APPLICANT: Hodgson, John APPLICANT: Knowles, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-24606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-252-991A-31958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-936-165A-506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
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                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-09-711-164-363
US-09-711-164-363
Sequence 363, Application US/09711164
Fatent No. 6589738
GENERAL INPORMATION:
APPLICANT: Ohlsen, Karl
APPLICANT: Ohlsen, Karl
APPLICANT: Ohlsen, Karl
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
CURRENT APPLICATION NUMBER: US 60/16415
FILE REFERENCE: 1999-11-0
CURRENT APPLICATION NUMBER: US 60/16415
FRICK APPLICATION NUMBER: US 60/16415
FRICK APPLICATION NUMBER: US 60/16415
FRICK SEQ ID NOS: 469
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 830
                                                                                                                                                                                          ;
0
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                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 241;
                                                                                                                                            Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                          9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                       Score 49; DB 3;
Pred. No. 13;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 VLILSAL---RRMLWAAD----DFLEDLPFEQIG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 LLLLTVLGLDRWMSWKTAPYIYDELQDLPYRQVG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 VLILSAL---RRMLWAAD----DFLEDLPFEQIG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48.5; DB Pred. No. 12; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48.5; DB
Pred. No. 12;
6; Mismatches
                                                                                                                                                                                                                                                                   118 DTLLYVASRNGLFAVENFLTEEPFQR 143
                                                                                                                                                                                                                                          6 DVLILSALRRMLWAADDFLEDLPFEQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8330, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Klebsiella pneumoniae US-09-489-039A-8330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.9%;
                                                                                                                                         29.2%;
nilarity 38.5%;
Conservative 7
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Best Local Similarity 38.2%;
Matches 13; Conservative
: 302 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Escherichia coli
US-09-711-164-363
                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                   Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-09-489-039A-8330
                                                                                              US-08-935-009A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 363
                                                                                                                                              Query Match
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g

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Score 47; DB 3; Length 312;
Pred. No. 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Burnham, Martin
APPLICANT: Burnham, Martin
APPLICANT: Lonetto, Michael
APPLICANT: Marren, Patrick
TITLE OF INVENTION: NOVEL 3-DEHYDROQUINATE SY
TITLE OF INVENTION: NIHASE
NUMBER OF SEQUENCES:
ADDRESSE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CONTRY: USA
CONTRY: USA
ZIP: 08543
COMPUTED PRICE AND PRICE
                                                                                             COURTER: IEM Compatible
COMPUTER: IEM Compatible
COMPUTER: FastSEQ for Windows Version 2.0
SOTTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,501
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/910,501
APPLICATION NUMBER: EFLIANG DATA:
APPLICATION NUMBER: 29,135
RETING DATE:
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: BLOOM, Allen
RESTRENCE/DOCKET NUMBER: 29,135
REFERENCE/DOCKET NUMBER: P50549-1
TELECOMMUTCATION INFORMATION:
TELEFRONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSBO for Windows Version 2.0
CURRENT APPLICATION DASS
APPLICATION NUMBER: US/08/910,501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: PS054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08910501
Patent No. 6020159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 312 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 DFLKTLPFEQI 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 DFLEDLPFEQI 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-910-501-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-08-910-501-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
APPLICANT: Nicholas, Richard
APPLICANT: Pratt, Julie
APPLICANT: Reichard, Richard
APPLICANT: Reichard, Richard
APPLICANT: Reichard, Ratin
APPLICANT: Rosenberg, Martin
APPLICANT: Rard, Judith
TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
TITLE OF INVENTION: Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.0%; Score 47; DB 3; Length 75; 81.8%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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Sequence 2, Application US/08910501

Fatent No. 6020159

Patent No. 6020159

Patent No. 6020159

Patent No. 6020159

Patent No. 6020159

TOTHE OF INVENTION:

MUMBER OF INVENTION: NOVEL 3-DEHYDROQUINATE SY

TITLE OF INVENTION: NTHASE

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

STATE:

STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PA

COMPUTER: PA

COMPUTER: 19406-0939

COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FeatSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A

FILING DATE: 24-SEP-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,032

FILING DATE: 24-SEP-1996

ATTORNEY/AGENT TRPORMATION:
NAME: Gimmi, Edward R

REGISTRATION NUMBER: 38,891

RECISTRATION NUMBER: 38,891

RECISTRATION NUMBER: 38,891

TELEPHONE: 610-270-4478

TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 DFLEDLPFEQI 32
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-936-165A-506
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```

0; Gaps

```
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TYPE: amino acid
; STRANDENESS: single
; TOPOLGOY: linear
US-08-910-501-4

Query Match
Best Local Similarity 81.8%; Score 47; DB 3; Length 312;
Best Local Similarity 81.8%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 1; Indels

Qy 22 DFLEDLPFEQI 32

Qy 162 DFLKTLPFEQI 172

Search completed: November 10, 2004, 13:44:00
Job time: 12.399 secs
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0; Gaps

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; Search time 35.4508 Seconds (without alignments) 328.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PCT_MBW_PUB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/RCT_MBW_PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/US06_NBW_PUB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/US06_NBW_PUB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: \cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: \cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

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16: \cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

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18: \cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1566620
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                 US-10-092-750-25
168
1 LDPVKDVLILSALRRMLWAADDFLEDLPFEQIG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1566620 seqs, 353225886 residues
                                                                                                                                                                                                         November 10, 2004, 16:36:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

2 T C A MMT 2

	Description	Sequence 25, Appl	Sequence 5837, Ap	Sequence 220, App	Sequence 141, App	Sequence 6676, Ap	Sequence 260441.	Sequence 259025,	Sequence 48632, A	Sequence 7605. Ap	Sequence 10933, A	Sequence 56875. A	Sequence 141820.	Sequence 70111, A
	ΩΙ	US-10-092-750-25	US-10-106-698-5837	US-10-755-889-220	US-10-097-340-141	US-10-739-930-6676	US-10-424-599-260441	US-10-424-599-259025	US-10-282-122A-48632	US-10-032-585-7605	US-09-815-242-10933	US-10-282-122A-56875	US-10-437-963-141820	US-10-282-122A-70111
	DB	14	14	16	14	11	15	15	15	14	6	15	16	15
	Query Match Length DB ID	33	98	444	413	473	67	346	481	1839	297	297	1030	1242
dю	Query	100.0	100.0	100.0	78.6	32.7	32.1	32.1	30.4	29.8	29.5	29.5	29.5	29.5
	Score	168	168	168	132	S	54	54	51	20	49.5	49.5	49.5	49.5
	Result No.	н	7	m	4	2	9	٠ ٦	80	σ	10	11	12	13

33

1 LDPVKDVLILSALRRMLWAADDFLEDLPFEQIG

8 8

RESULT 2
US-10-6-698-5837
Sequence 5837, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:

5 29.5 1404 9 US-09-811-045A-1	Sednence
49 29.2 323 15 US-10-282-122A-69	oe sednence
6 49 29.2 510 14 US-10-104-047-3594	Sednence
7 4 4 29.6 92.9 9 08-09-738-828-3808	sednence
6 49 29.2 TOTA 16 US-10-437-963-113343	43 sequence
0 49 29 2 1429 10 HS-09-912-473-0	Sequence 3, Appii
1 49 29 2 1429 12 TR2-10-087-1608	and
2 49 29.2 1429 17 118-10-714-228-14	Semience
3 49 29.2 1453 14 US-10-371-857-21	Sequence 21. Appl
4 49 29.2 1545 15 US-10-114-270-174	Semience 174. Ann
5 49 29 2 1821 16 118-10-437-963-203003	O3 Semience
6 49 29.2 2333 16 IIS-10-437-963-138446	46 Segment
7 48.5 28.9 187 14 US-10-182-504-26	enternes.
48.5 28.9 239 14 US-10-287-274-363	Sequence 363. Ann
9 48.5 28.9 507 16 US-10-437-963-145784	84 Semence
0 48.5 28.9 1234 14 US-10-369-493-18637	7 Semience
1 48.5 28.9 1990 15 113-10-262-839-146	o creinstean
2 48 28.6 303 14 115-10-156-761-9163	901191598
3 48 28 6 394 16 TIS-10-437-963-151727	27 Semience
4 48 28 K 1503 14 110-10-437-063-144201	2) Sequence
100f0f-006-/0f-01-00 of 000f 0:07 of 0	action to
700000 1:1 107 0: 01 175 0: 07 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	seduence
7 47.0 20.0 14 I/ OS-IO-420-IIO-22041	sequence
7.75 20.5 12.5 10 US-LU-701-701-62.689	y sequence
74 78.0 TT 0 T	ri sednence
75 47 78.0 7 05.03.03.03.939.980-506	sednence
1 47 28.0 //0 14 US-10-369-493-18281	Sequence
1 4/ 28.0 1009 IS US-10-654-416-I	ednence
2 46.5 27.7 282 13 US-10-136-253-7	Sequence
3 40 T 27.7 6/3 T/ OB-LU-/38-930-5555	sednence
7.7.7	82 Sequence
0 1.4 50 LS US-IU-424-599-I/446	es seguence
ALIGNMENTS	
5, Application	
03003	
CONTRACT INFORMATION IN	
. DDDITCANT. Diric Tilis	
DEDITORNAL ENTREM NATION	
. TITE OF INVENTION. Dolumentides Interscrine with DCL.V.	
FILE REFERENCE: 50036/050002	
CURRENT APPLICATION NUMBER: US/10/092.750	
; PRIOR APPLICATION NUMBER: US 60/274,526	
PRIOR FILING DATE: 2001-03-08	
; NUMBER OF SEQ ID NOS: 253	
; SOFTWARE: FastSEQ for Windows Version 4.0	
; SEQ ID NO 25	
E !	
; OKGANISM: Homo sapiens	
7-06/-760-01-6	
tch 100.0%; Score 168; DB 1	
Similarity 100.0%; Pred. No. 1.8e-17;	
33; Conservative 0; Mismatches 0	; Indel

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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Nucleic Acid Molecules and Therapy of Ovarian Cancer
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFRENCES: MRI-030
CURRENT PAPLICATION NUMBER: US/10/097,340
CURRENT PILING DATE: 2002-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-16
PRIOR PRIOR SEQ ID NOS: 363
PRIOR FILING DATE: 2001-03-16
PRIOR PRIOR PRIOR DATE: 2001-03-16
PRIOR PRIOR DATE: 2001-03-16
PRIOR PRIOR PRIOR DATE: 2001-03-16
PRIOR PRIOR DATE: 2001-03-16
PRIOR PRIOR DATE: 2001-03-16
PRIOR PRIOR DATE: 2001-03-16
PRIOR PRIOR DATE: 2001-03-19
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Publication No. US20040216190A1

GENERAL INFORMATION:

APPLICANT: KOVAULC.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

FILE REFERENCE 38-21(53377)B

CURRENT FILING DATE: 2003-12-18

HUMBER OF SEQ ID NOS: 11088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 78.6%; Score 132; DB 14; Best Local Similarity 78.8%; Pred. No. 6.3e-11; Matches 26; Conservative 4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||:||:||:||||||||:|
371 LDPMKDILILSALRQMLRAADDFLEDLPLEETG 403
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ORGANISM: Arabidopsis thaliana
                                                     Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
                                                                                                                                                    Rosemarie SCHMANDT
                                                                                                                                                                                  Xumei ZHAO
Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                          eter VEIBY
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US-10-739-930-6676
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT APPLICATION NUMBER: US/202-203-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: US 60/163,280
NUMBER OF SEQ ID MOS: 8564
SOFTWARE: PATENTING NOS: 8564
SOFTWARE: PATENTING US 8564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 220, Application US/10755889
; Sequence 220, Application US20040171823A1
; Sequence 220, Application No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT BETSECL PETSECTION POLYWICLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFRENCE: DO294 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT PILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR PILING DATE: 2003-01-14
; RIOR APPLICATION NUMBER: U.S. 60/469,757
; NUMBER OF SEQ ID NOS: 823
; SEQ ID NOS: 823
; SEQ ID NOS: 823
; SEQ ID NO 220
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100.0%; Score 168; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 168; DB 14
Best Local Similarity 100.0%; Pred. No. 5.1e-17
Matches 33; Conservative 0; Mismatches 0
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Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manjula GANNAVARAPU
Sebastian HOERSCH
Shubhangi KAMATKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rachel E. MEYERS
Michael MORRISEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steve G. KOVATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
GORGANISM: Homo sapiens
US-10-755-889-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-106-698-5837
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LENGTH: 86
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APPLICANT:
APPLICANT:
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Sequence 7005, Application US/10032585

Publication No. US20030180953A1

Sequence 7005, Application US. US20030180953A1

Sequence 7005, Application No. US20030180953A1

SEQUENCANT: Terry, Roemer D.

APPLICANT: Bo, Jiang

APPLICANT: Howard, Busone

CURRENT APPLICANT: 10182-005-999

CURRENT APPLICANTON NUMBER: US/10/032,585

CURRENT PILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SOFTWARE: Patentin version 3.1

SEQ ID NO 7605

LENGTH: 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-65
PRIOR PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-11-2-2
PRIOR PLING DATE: 2000-11-2-2
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PR
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, Trawick, Robert
APPLICANT: Yanamoto, Robert
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITARA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
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Best Local Similarity 50.0%; Pred. No. 73;
Matches 11; Conservative 6; Mismatches 5; Indels
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Pred. No. 4.5e+02;
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35.5%;
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// ORGANISM: Candida albicans
US-10-032-585-7605
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Best Local Similarity
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                                                                               Sequence 260441, Application US/10424599
Sequence 260441, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Thou Yihua
APPLICANT: Caro Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21 (53223)
CURRENT APPLICATION NUMBER: US/10/424,599
UNDRER OF SEQ ID NOS: 285684
SEQ ID NO 260441
SEQ ID NO 260441
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cavalic David K
APPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.1%; Score 54; DB 15; Length 67; Best Local Similarity 45.7%; Pred. No. 2.9; Matches 16; Conservative 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_77200C.1.pep
US-10-424-599-260441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
, OTHER INFORMATION: Clone ID: PAT_MRT3847_75923C.1.pep
US-10-424-599-259025
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-10-424-599-259025
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US-10-282-122A-48632
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Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essentia FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-10-23
PRIOR PRIOR DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
29.5%; Score 49.5; D
Best Local Similarity 40.7%; Pred. No. 71;
Matches 11; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 141820, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Vinua
APPLICANT: Cao, Yinua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Butharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 DVLILSALRRMLWAADDFLEDLPFEQI 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Enterococcus faecalis US-10-282-122A-56875
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Best Local Similarity 34.0%;
Matches 17; Conservative
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APPLICANT:
APPLICANT:
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                    Gaps
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                    Indels
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ITLE OF INVENTION: Identification of Essential Genes in
ITLE OF INVENTION: Prokaryotes
                                                                                                    1639 VKSVIQLLLIQSLSELFESDDFYENVPYDYL 1669
                                                                    4 VKDVLILSALRRM--LWAADDFLEDLPFEQI 32
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Best Local Similarity 40.7%; Pred. No. 71;
Matches 11; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR PELLING DATE: 2001-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-12-27
PRIOR PELLING DATE: 2000-12-27
PRIOR PELLING DATE: 2001-12-27
PRIOR PELLING DATE: 2001-12-27
PRIOR PELLING DATE: 2001-12-27
PRIOR PELLING DATE: 2001-12-26
PRIOR PELLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FESSEQ for Windows Version 4.0
                    10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |:|:| ::: || ::: || ||: DILVINAAQQISCAA---IEELPMEQV 155
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                  Sequence 10933, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10933
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Forsyth, R.
                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILE REFERENCE: ELITRA.011A
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Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                       Matches
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APPLICANT: Lift Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION: US/163211) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
SEQ ID NOS: 204966
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 56875
LENGTH: 297
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                                                                                                                                                                                                                                                           DB 15; Length 297;
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US-10-437-963-141820
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Pred. No. 2.8e+02;
6; Mismatches 10;
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US-10-282-122A-69906
; Sequence 69906, Application US/10282122A
; Sequence 69906, Application US/10282122A
; Publication No. US20040029129A1
; APPLICANT: Wang, Liangsu
; APPLICANT: Amalone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Glisen, Kari
; APPLICANT: Olisen, Kari
; APPLICANT: O'Skind, Judith
                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Unknown
FEATURE:
NAME/KEY: PEPTIDE
OTHER INFORMATION: P2P polypeptide
US-09-811-045A-1
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT:
APPLICANT:
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APPLICANT: Franch
APPLICANT: Frest, Grant
APPLICANT: FORSYth, R.
APPLICANT: APPLICATION: Identification of Essential Genes in Microorganisms
FILE OF INVENTION: Identification of Essential Genes in Microorganisms
CURRENT FILING DATE: 2003-02-20
FRIOR PAPLICATION NUMBER: 60/206,848
FRIOR FILING DATE: 2000-05-23
FRIOR APPLICATION NUMBER: 60/200,727
FRIOR APPLICATION NUMBER: 60/200,727
FRIOR PELING DATE: 2000-05-26
FRIOR PAPLICATION NUMBER: 60/200,727
FRIOR PELING DATE: 2000-09-09
FRIOR PELING DATE: 2000-09-09
FRIOR PELING DATE: 2000-10-23
FRIOR APPLICATION NUMBER: 60/25,625
FRIOR APPLICATION NUMBER: 60/25,625
FRIOR APPLICATION NUMBER: 60/25,636
FRIOR PELING DATE: 2000-10-23
FRIOR PELING DATE: 2000-10-23
FRIOR PELING DATE: 2001-02-09
FRIOR PELING DATE: 2001-02-16
FRIOR DATE: 2001-03-16
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Patent No. US20020035080A1
GENERAL INFORMATION:
APPLICANT: Scott, Robert E.
TITLE OF INVENTION: cDNA encoding P2P proteins and use of P2P cDNA-
TITLE OF INVENTION: derived antibodies and antisense reagents
TITLE OF INVENTION: in determining the proliferative potential of
                                   1;
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                                                                                                                                                                                                           Sequence 70111, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
1 LDPVKDVLILSALRRM----LWAADDF-
                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ollsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pseudomonas syringae
US-10-282-122A-70111
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Best Local Similarity 42.3-
                                                                                                                                                 RESULT 13
US-10-282-122A-70111
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US-09-811-045A-1
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ORGANISM:
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FILE REPERENCE: ELITEA, 034A

CURRENT APPLICATION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITEA, 034A

CURRENT FILMS DATE: 2003-02-20

FRICA APPLICATION NUMBER: 6/191,076

PRICA FILING DATE: 2000-03-21

PRICA FILING DATE: 2000-05-26

PRICA FILING DATE: 2000-05-26

PRICA FILING DATE: 2000-05-26

PRICA FILING DATE: 2000-05-26

PRICA PLICATION NUMBER: 6/230,335

PRICA PLICATION NUMBER: 6/230,335

PRICA PLICATION NUMBER: 6/220,335

PRICA FILING DATE: 2000-09-06

PRICA PLICATION NUMBER: 6/223,325

PRICA PLICATION NUMBER: 6/223,625

PRICA PLICATION NUMBER: 6/257,931

PRICA PLICATION NUMBER: 6/257,931

PRICA PAPLICATION NUMBER: 6/267,636

PRICA PLICATION NUMBER: 6/267,636

PRICA PLICATION NUMBER: 6/269,308

PRICA PLICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
TITLE OF INVENTION: normal, abnormal and cancer cells in animals FITLE OF INVENTION: and humans FITLE OF INVENTION: and humans CURRENT PEFERENCE: D63860 CURRENT APPLICATION NUMBER: US/09/811,045A PRIOR APPLICATION NUMBER: US 08/801,308 PRIOR FILING DATE: 1997-02-18 PRIOR FILING DATE: 1997-02-18 SEQ ID NOS: 4

LENGTH: 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.5%; Score 49.5; DB 9; Length 1404; Best Local Similarity 31.6%; Pred. No. 4e+02; Matches 12; Conservative 8; Mismatches 11; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1094 PAEDVIIMIQVPQSKWDKDDFESEEEDVKTTQPIQSVG 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PVKDVLILSALRRMLWAADDF---LEDL----PFEQIG 33
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7

; ORGANISM: Pseudomonas syringae US-10-282-122A-69906

Query Match 29.2%; Score 49; DB 15; Length 323; Best Local Similarity 44.8%; Pred. No. 92; Matches 13; Conservative 5; Mismatches 7; Indels

1 LDPVKDVLILSALREMLWAADDFL-EDLP 28

g à

Search completed: November 11, 2004, 01:28:07 Job time: 36.5008 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 12:29:32; Search time 7.35233 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

US-10-092-750-25 168 1 LDPVKDVLILSALRRMIWAADDFLEDLPFEQIG 33 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P44 hebatitis-asso	rotubular	ö		centromere k-type	hypothetical prote	H	genome polyprotein	uracil phosphoribo	probable retroelem	glia maturation fa	06-methylquanine-D	O6-methylguanine-D	threonine synthase	gene ND1 intron 3	hypothetical prote	.H+-transporting tw	hypothetical prote	hypothetical prote	hypothetical prote	methylated-DNA-[pr	UL44 protein - hum	hypothetical 49.9	al	2.14		prot	ij	vancomycin resista	
SUMMARIES	QI	69	821	D96591	480	921	465	A45540	RRWPEM	G72341	B84504	JC6308	H85860	F91016	SYBSR	806057	T26371.	S01401	B86050	H91203	T42683	XYECO2	QQBEV2	A65168	AH1889	B96682	A11901	139732	G64982	AF0780	
	DB	-	~	7	7	~	7	N	Н	~	~	7	~	~	Н	N	N	N	N	N	N	Н	М	N	N	ď	0	7	Н	7	
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•	* Query Match	100	100.0	32.7	'n	ď	ď	н	Ξ.	Ξ.	ö	φ.	ď	ο.	φ.	σ,	σ.	ď	φ.	φ.	٥.	φ.	φ.	φ.	φ.	σ,	œ,	œ.	m.	m.	
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	Result No.		0	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	50	

vancomycin sensiti	vancomycin sensiti	hypothetical prote	conserved hypothet	hypothetical prote	cobalamin biosynth	proliferation pote	hypothetical prote	hypothetical prote	mannose-6-phosphat	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	probable retroelem	hypothetical prote
F85852	D91008	T26828	H83090	S42385	A84310	T42727	AD1825	C87706	A86721	D83142	AD3028	G98256	S77190	G84516	T50609
~	N	N	~	N	N	N	N	N	N	N	~	7	7	~	~
239	239	245	364	589	1234	1560	81	279	315	335	513	513	717	1466	529
28.9	28.9	28.9	28.9	28.9	28.9	28.9	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.3
48.5	48.5	48.5	48.5	48.5	48.5	48.5	48	48	48	48	48	48	48	48	47.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

T TOOOK
n.50.0 P44 heatitis-associated anticen - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 07-May-1999
:
Kitakahashi, K.; Kutamura, N.; Shibui, T.; Kamizono, M.; Matsui, K.; Yoshiyama, Y.; Maeda J. Gen. Virol. 71. 2005-2011. 1990
A, Title: Cloning, sequencing and expression in Escherichia coli of cDNA for a non-A, non-
A; Reference number: A43676; MUID: 91011346; FMID: 2170570
A/ACCESSION: A456 /6
A, Molecule type: mRNA
A;Residues: 1-444 <tak></tak>
Kihonda, Y.; Kondo, V.; Madda, T.; Yoshiyama, Y.; Yamada, E.; Shimizu, Y.K.; Shikata, T.; T. Gen Vivrl 71 1990-2014 1900
A;Title: Isolation and purification of a non-A, non-B hepatitis-associated microtubular a
A43677; MUID:91011345; PMID:2170569
. A,Accession: A43677
A Status: preliminary
A;Residues: 14-22;108-128;200-214;231-240 <hon></hon>
Pred. No. 1.6e-16; 0; Mismatches 0; Indele
Qy 1 LDPVXDVLLLSALRRMLWAADDFLEDLPFEQIG 33
D\$ 398 LDPVXDVLILSALRRMLWAADDFLEEDLPFEQIG 430
microtubular aggregate protein - human
 C; Species: Home sapiens (man)
 C.bace: labout 1999 #sequence revision is-Oct-1999 #text_change is-Oct-1999 C.bacession: S4821#
R; Kitamura, A.; Takahashi, K.; Okajima, A.; Kitamura, N.
Eur. J. Biochem, 224, 877-883, 1994
A.Title: Induction of the human gene for p44, a hepartits-C-associated microtubular aggre
Affected number: S40210; MOID:30010070; FMID:7925411 Affects: S448118 Affects: profilming.
 A,Molecule type: DNA A,Molecule type: DNA A,Residues: 1-444 <kit></kit>
 Query Match 100.0%; Score 168; DB 2; Length 444;
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Gaps

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Filin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.; Kaul, S.; Kaul, S.; Cronin, L.A.; Shen, M.; WanAken, S.E.; Umayam, L.; Tallon, L.; enss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Accession, A84652
A;Accession, A84652
A;Accession a84652
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39217
R;Mobougall, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
R;Mobougall, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
R;Reference number: Z21836
A;Reference number: Z21836
A;Reseasion: T39217
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-514 <MCD>
A;Residues: 1-514 <MCD>
A;Residues: 1-514 scorp.
A;Residues: 1-514 scorp.
C;Genetics: Sxperimental source: strain 972h-; cosmid c9E9
C;Genetics: C;Genetics: Sxperimental source: strain 972h-; cosmid c9E9
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A,Molecule type: genomic RNA
A,Residues: 1-178 «JAC.
A,Residues: 1-178 «JAC.
A,Cross-references: UNIPROT:P36352; GB:S97776; NID:G248382; PIDN:AAB21996.1; PID:g248383
A,Cross-references: UNIPROT:P36352; GB:S97776; NID:G248382; PIDN:AAB21996.1; PID:g248383
A,Note: sequence extracted from NCBI backbone (NCBIN:97776, NCBIP:97778)
A,Note: in Genbank entry S97776, release 109.0, the source is designated as Belladonna mc
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A,Cross-references: UNIPROT:Q95L90; GB:AE002093; NID:g4874311; PIDN:AAD31373.1; GSPDB:GNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein At2g25730 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: A64652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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A,Map position: 1
C,Superfamily: human transposon MER37 probable transposase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
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Pred. No. 4
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DQVHEVAIISVLRRILKRLQEFLE 884
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50.0%;
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Matches 12; Conserv
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A;Map position: 2
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                                                                                                                                                                                                                                                                                                                 C;Accession: D95591

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Residues: 1-473 <STO>
A.Residues: 1-473 <STO>
A.Cross-references: UNIPROT.Q9FZ33; GB:AE005173; NID:g9857523; PIDN:AAG00878.1; GSPDB:GN
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
Molecule type: DNA
A;Residues: 1-378 <STO>
A;Cross-references: UNIPROT:Q9ZVH8; GB:AE002093; NID:g3786016; PIDN:AAC67362.1; GSPDB:GN
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C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C,Accession: E84806
                                                                                                                                                                                                                        hypothetical protein T24C10.10 (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                              1 LDPVKDVLILSALRRMLWAADDFLEDLPFEQIG 33
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177 VKEVYGLIQEKGVFWAFDQMIETGDLPYEBI 207
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Pred. No. 4.6;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VKDVLILSALRRMLWAADDFLE--DLPFEOI 32
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ilarity 41.9%;
Conservative 6
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ilarity 31.4%;
Conservative 8
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Best Local Similarity
Matches 13; Conserv
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Matches 16; Conserv
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Molecule type: DNA
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A;Gene: T24C10.10
A;Map position: 1
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A;Map position: 2
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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; h. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9SKG3; GB:AE002093; NID:g4432801; PIDN:AAD20653.1; GSPDB:GN(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85860
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Mature 409, 529-533, 201
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-354 <STO>
A;Cross-references: UNIPROT:Q8XE42; GB:AE005174; NID:g12516548; PIDN:AAG57348.1; GSPDB:GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies: Brugia malayi
Cispecies: Brugia malayi
Cipate: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 17-Mar-1999
Cipate: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 17-Mar-1999
Rill, L.X.; Xu, H.; Weller, P.F.; Shi, A.; Debnath, I.
Gene 186, 1-5, 1997
A;Titler: Structure and expression of a novel filarial gene for glia maturation factor. A;Reference number: JC6308; MUID:97199361; PMID:9047337
A;Reference tructure and expression of a hovel filarial gene for glia maturation factor. A;Reference number: JC6308
A;Reference number: JC63
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                                                                                                    probable retroelement pol polyprotein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: B94504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 6.8;
3; Mismatches
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C;Superfamily: glia maturation factor beta
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Best Local Similarity 46.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-411 <STO>
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Accession: B84504
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A, Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alternate polyprotein - eggplant mosaic virus
NyAlternate names: RNA mucleotidyltransferase (RNA-directed); RNA replicase
NyContains: RNA-mucleotidyltransferase (EC 2.7.7.48)
Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: eggplant mosaic virus
C;Species: gegplant mosaic virus
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 19-Jan-2001
C;Accession: JO012
R;Osorio-Keese, M.E.; Keese, P.; Gibbs, A.
Virology 172, 547-554, 1989
A;Title: Nuclectide sequence of the genome of eggplant mosaic tymovirus.
A;Accession: J00102
A;Molectide sequence of the genome of eggplant mosaic tymovirus.
A;Accession: J00102
A;Molectide sequence of the genome of eggplant mosaic tymovirus.
A;Accession: J00102
A;Molectide sequence of the genome of eggplant mosaic virus RNA-directed RNA polymerase
C;Superfamily: eggplant mosaic virus RNA-directed RNA polymerase
C;Superfamily: eggplant mosaic virus RNA-directed RNA polymerase
C;Superfamily: eggplant mosaic virus motif A (P-loop)
F;955-972/Region: nucleotide-binding motif A (P-loop)
F;957-1032/Region: nucleotide-binding motif B
F;971/Binding site: ATP (Lys) #status predicted
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Uracil phosphoribosyltransferase - Thermotoga maritima (strain MSB8)

C;Species In-thermotoga maritima
C;Date: 11-Uun-1999 #sequence_revision 11-Uun-1999 #text_change 09-Jul-2004
C;Accession: G7241
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A;Accession: G72341
A;Accessio
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C;Superfamily: eggplant mosaic virus RNA-directed RNA polymerase C;Keywords: ATP
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Pred. No. 44;
6; Mismatches 12; Indels
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                                                                                                                                             Length 178
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                                                                                                                                             Score 53; DB 2;
Pred. No. 3.3;
9; Mismatches 1
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Pred. No. 5.5;
5; Mismatches
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ilarity 35.7%;
Conservative
                                                                                                                                        Query Match
Best Local Similarity 29.6%;
Matches 8; Conservative
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Best Local Similarity 41.4%;
Matches 12; Conservative
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Matches 10; Conserva
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Best Local Similarity 35.55
Matches 11; Conservative
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A,Genetic code: SGC3
C,Keywords: mitochondrion
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S06057
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NyAlternate names: protein YCR053w
CiSpecies: Saccharomyces cerevisiae
CjDate: 31-Dec-1992 #sequents and an analysis of the yeast cinden, G.; Vetter, I.; Maurer, K.; Pilz, U.; Planta, R.; Feldm R; Mannhaupt, G.; van der Linden, G.; Vetter, I.; Maurer, K.; Pilz, U.; Planta, R.; Feldm A; Title: Analysis of the THR4 region on chromosome III of the yeast Saccharomyces cerevial A; Reference number: S22836; MUD:90371958; PMID:2204248
                                                                                          A,Gene: ada
C,Superfamily: adaptive response regulatory protein; methylated-DNA-protein-cysteine S-m
C,Keywords: methylated amino acid
F,321/Binding site: methyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Escherichia coil
C;Species: Escherichia coil
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F91016
C;Accession: F91016
R;Hayashi, T; Makinc, K; Ohnishi, M; Kurokawa, K; Ishii, K; Yokoyama, K; Han, C.G. gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, H. DNA Res. B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc A;Accession: F91016
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A, Residues: 1-514 cAMA>
A, Residues: 1-514 cAMA>
A, Cross-references: UNIPROT:P16120; EMBL:X59720; NID:g1907116; PIDN:CAA42284.1; PID:g190
R, Aas, S.F.; Rognes, S.E.
Nucleic Acids Res 18, 65, 190
A, Title: Notleoride sequence of the yeast THR4 gene encoding threonine synthase.
A, Reference number: S20154; MUID:90175003; PMID:2408022
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A,Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: EMBL.X17256; NID:94615; PIDN:CAA35157.1; PID:94616
R,van der Linden, C.G.; Maurer, C.T.C.; Planta, R.J.; van Vliet-Reedijk, J.C.; Vreken,
submitted to the Protein Sequence Database, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F91016
O6-methylguanine-DNA methyltransferase [imported] - Bscherichia coli (strain O157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: ECs3102
C,Superfamily: adaptive response regulatory protein; methylated-DNA-protein-cysteine
C,Keywords: methylated amino acid
F;321/Binding site: methyl (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                Length 354;
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                                                                                                                                                                                                                                                                                                       9; Indels
A, Experimental source: strain O157:H7, substrain EDL933 C, Genetics:
                                                                                                                                                                                                                                         13. Score 50; DB 2; 11arity 42.3%; Pred. No. 19; Conservative 6; Mismatches
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42.3%; Pred. No. 19;
vative 6; Mismatches
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Best Local Similarity
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-354 <HAY>
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A;Residues: 1-514 <AAS>
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A;Reference number: S19415
A;Accession: S19467
A;Accession: S19467
A;Accession: S19467
A;Accession: S19467
A;Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42284.1; PID:g1907196; GSPDB:GN006
G;Genetics: GGD:THH4; MIPS:YCR053w
A;Cross-references: SGD:S0000649; MIPS:YCR053w
A;Cross-references: SGD:S0000649; MIPS:YCR053w
A;Cross-references: SGD:S0000649; MIPS:YCR053w
C;Superfamily: threonine synthase
C;Keywords: carbon-oxygen lyase; phosphoprotein; pyridoxal phosphate; threonine biosynthe
F;124/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cummings, D.J.; Domenico, J.M.; Michel, F.
Curr. Genet. 14, 253-264, 1988
Curr. Genet. 14, 253-264, 1988
A;Title: DNA sequence and organization of the mitochondrial ND1 gene from Podospora anser A;Reference number: S06056; MUID:89063443; PMID:3197134
A;Accession: S06057
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C;Species: mitochondrion Podospora anserina
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: S06057
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                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
29.8%; Score 50; DB:
Best Local Similarity 38.9%; Pred. No. 29;
Matches 14; Conservative 6; Mismatches
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A;Residues: 1-580 <CUM>
A;Cross-references: UNIPROT:Q02714; EMBL:X13164
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Pred. No. 3
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Q9w366 drosophila Q6d5p8 erwinia car Q8ke34 chlorobium Q9skg3 arabidopsis Q8a6bb arabidopsis Q8a6bb arabidopsis Q865g6 caenorhabdi Q9Gx2 chayote mos Q9rdg9 streppomyce Q9rdg9 streppomyce Q1417 solanum dem Aat39966 solanum d Q8aa59 mus musculu G9aik8 pseudomonas

09W366 06DSP8 06DSP8 09SKG3 08S8B3 08SB3 08A60 09A17 04117 04117 04117 06L417 06L417 06L417

ALIGNMENTS

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November 10, 2004, 12:27:34; Search time 40.2953 Seconds (without alignments) 471.205 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                             - protein search, using sw model
                                                                                          OM protein
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US-10-092-750-25 168 1 LDPVKDVLILSALRRMLWAADDFLEDLPFEQIG 33 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 Total number of hits satisfying chosen parameters: 1825181 seqs, 575374646 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Ostcb0 homo sapien	()	homo	Q99984 homo sapien	homo	mus n	mus	Q8bv66 mus musculu	Q9er37 mus musculu	Q9bdb7 mus musculu	Q6y224 pagrus majo	Aap20189 pagrus ma	Q8t749 branchiosto	Q6nm08 arabidopsis	Aas76264 arabidops	ы						513	schizos			P36352 physalis mo			œ	P20126 eggplant mo	Q9wzi0 thermotoga
Ω	IF44 HUMAN	IF44 PANTR	Q144 <u>9</u> 6	Q99984	Q96B64	Q8SP46	Q8R0G4	QBBV66	Q9ER37	Q9BDB7	Q6Y224	AAP20189	Q8T749	Обимов	AAS76264	Q8VXZ6	085707	094407	Q9FZ33	Q9ZVH8	093561	089513	CBH1_SCHPO	Q7QBS5	Q9SL90	POLR PHMV	Q89D37	Q72JY5		POLR EPMV	.UPP_THEMA
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398 LDPVKDVLILSALRRMLWAADDFLEDLPFEQIG 430
                              1 LDPVKDVLILSALRRMLWAADDFLEDLPFEQIG 33
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Q14496
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver,
MEDLINE=91011346; PubMed=2170570;
Takahashi K., Kitamura N., Shibui T., Kamizono M., Matsui R.,
Takahashi K., Kitamura T., Kondo J., Honda Y., Yamada E., Shimizu Y.K.,
Yoshiyama Y., Nakanishi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
15-UUL-2004 (Rel. 44, Last annotation update)
1 Interferon-induced protein 44 (Antigen p44) (Non-A non-B hepatitis-
associated microtubular aggregates protein).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                             100.0%; Score 168; DB 1; Length 444; 100.0%; Pred. No. 1.2e-15; rive 0; Mismatches 0; Indels C
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Antigen; Direct protein sequencing.
SEQUENCE 444 AA; 50471 MW; 799CC855018CFA71 CRC64;
                                                                                                                                                                     444 AA; 50461 MW; BC26CA9D7CE41F2F CRC64;
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100.0%; Score 168; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 33; Conservative 0; Mismatches 0;
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                                                                    EMBL; BC022870; AAH22870.; --
Genew; HGNC:16938; IF144.
Interferon induction.
SEQUENCE 444 AA. EA.
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P27473;
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IF44 PANTR
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TISSUE-Cancellous bone;
Ohno I., Hashimoto J., Takaoka K., Ochi T., Okubo K., Matsubara K.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
BENBL, AB000115; BAA19056.1; -.
SEQUENCE 413 AA, 46933.MW; 026A6813174E530F CRC64;
                                                                                                                                                                                                                                                                                             MEDININE-95010078; PubMed=7925411;

A Kitamura A., Takahashi K., Okajima A., Kitamura N.;

Kitamura A., Takahashi K., Okajima A., Kitamura N.;

Tinduction of the human genee for p44, a hepatitis C-associated

I mirrotubular aggregate protein, by interferon-alpha/beta.";

Eur. J. Bloochem. 224:877-883(1994).

R EMBL; D28916; BAA06043.1; JOINED.

R EMBL; D28910; BAA06043.1; JOINED.

R EMBL; D28911; BAA06043.1; JOINED.

R EMBL; D28912; BAA06043.1; JOINED.

R EMBL; D28913; BAA06043.1; JOINED.

R EMBL; D28914; BAA06043.1; JOINED.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Hepatitis C-associated microtubular aggregate protein P44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
HOMO sapiens MRNA expressed in osteoblast, complete cds.
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GO; GO:0009615; P:response to virus; TAS.
SEQUENCE 444 AA; 50502 MW; 39B7D8DA0F3F6DE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 168; DB 2;
100.0%; Pred. No. 1.2e-15;
iive 0; Mismatches 0;
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444 AA
PRT;
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                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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  PRELIMINARY;
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Matches 26; Conservat
                                                                                                                                                      Homo sapiens (Human)
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Best Local Similarity
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Q14496;
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Q99984;
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SEQUENCE
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OBROG4;
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Q8R0G4
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Alausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

Bapleton M., Soares M.B., Bonaldo M.F., Carninci D., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci D., Prange C.,

Raha S.S., McEwan P.J., McKernan K.J., Marke J.A., Gunaratne P.H.,

Roass S.A., McEwan P.J., McKernan K.J., Marke J.A., Gunaratne P.H.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rach J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mniting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Antiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,

"Marra M.A.,

"Marra M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CZECH II;
TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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78.8%; Pred. No. 1.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew, HGNC:17817, Clor£29.
SEQUENCE 413 AA, 46926 MM, AF146D9ECD006EEB CRC64;
                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to histocompatibility 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LOPVKDVLILSALRRMLWAADDFLEDLPFEQIG 33
                                                                                                                                             413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 AA.
                                                                                                                                                                                                                     Created)
                                                                                                                                             PRT;
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                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel, 19, 01-DEC-2001 (TrEMBLrel, 19, 01-MAR-2003 (TrEMBLrel, 23, Histocompatibility 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (OCT-2001) to the
EMBL; BC015932; AAH15932.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.
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                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       Name=Clorf29;
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Q8SP46;
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Q8SP46
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RARRANCO CORDITATOR

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Expression driven by an wMTV-LTR enhancer.;

XX MEDINE=228825; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XA Strausberg R.L., Schomen C.M., Schuler G.D.,

XA Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Antschul K., Farmer A.A., Rubin G.M., Hong L.,

XA Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H.,

XA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.W., Sodergien E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

XA Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22389257; PubMed=12477932;

X STRAIN-MILL YEAVINGT. WAP-TGF alpha model. 7 months old;

X RETUINE-22389257; PubMed=12477932;

A StrainSerg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Rapha S.S., Loqquellano N.E., Poraldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loqquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Expression driven by an MMTV-LTR enhancer.;
Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-UNAR-2004 (TrEMBLrel. 26, Last annotation update)
A430056A10Rik protein (Fragment).
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Pred. No. 2.8e-07;
6; Mismatches 6
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Best Local Similarity 63.6%;
Matches 21; Conservative
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Mus musculus (Mouse).
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Best Local Similarity
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Q9ER37
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STRAIN=C57BL/6J; TISSUE=Thymus;
STRAIN=210499374; PubMed=11042159;
MEDLINE=2104999374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002)
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
library, clone:A430056A10 product:MICROTUBULE ASSOCIATED PROTEIN 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=mix FVB/N;
TISSUE=mnummary tumor. WAP-TGF alpha model. 7 months old;
Strausberg R.;
Strausberg (A.R.-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC026901; AAH26901.1;
MGD; MGI:2443016; A430056Al0Rik.
                                                                                                                                                                                                                                                                                                                        SEQUENCE 115 AA; 13159 MW; 86AD44C8495224DD CRC64;
                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                               63.1%; Score 106; DB 2;
64.5%; Pred. No. 2.8e-07;
ive 7; Mismatches 4;
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MEDLINE=9927923; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LDPVKDVLILSALRRMLWAADDFLEDLPFEQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422 AA
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MEDLINE-21085660; PubMed=11217851;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
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Meth. Enzymol. 303:19-44(1999)
                                                                                                                                                                                                                                                                                                                                                                                                               20; Conservative
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Name=A430056A10Rik;
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OBBV66

OBBV6

OBBV6

OB 10-M

OB 10-M
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Thymus;

Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Fukuda S., Furuno M., Hiramoto K., Hiraoka T., Hirozane T.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

A Katoh H., Kawai J., Solima Y., Sakazume N., Ohason N., Okazaki Y.,

A Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Saito R., Saltoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Submitted (Apr. 2002) to the BMBL/GenBank/DDBJ databases.

B MGD; MGI:2443016; A430056410Ri.

GO; GO:0003779; F:actin binding; IEA.

GO; GO:000710; P:cytoskeleton, IEA.

R D; GO:000710; P:cytoskeleton organization and biogenesis; IEA.

S InterPro; IPRO02097; Profilin:

S InterPro; IPRO02097; Profilin:

S InterPro; IPRO02097; Profilin:

S InterPro; IPRO02097; Profilin:
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MEDLINE-20530913; PubMed=11076861; Rischell Risc
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Sciurognathi, Muridae, Murinae, Mus.
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ299405; CAC13979.1; -
MMGD; MG1:2443016; A430056A10Rik.
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0003779; F:actin binding; IEA.
GO; GO:0007010; P:cytoskeleton organization and biogenesis;
InterPro; IPR002097; Profilin.
SEQUENCE 422 AA; 47880 MW; F267831AA0054856 CRC64;
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Last annotation update)
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Pred. No. 1.1e-06;
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Pred. No. 1.1e-06;
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64.5%; Pred. No. 1...
7; Mismatches
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01-MAR-2001 (TrEMBLrel. 16, Last seqt
01-MAR-2004 (TrEMBLrel. 26, Last ann
Microtubule associated protein 44.
Name=A430056A10Rik; Synonyms=Mtap44;
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Mammalia; Eutheria; Rodentia;
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es 20; Conservative
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